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(54) Title: **NON-TRANSGENIC HERBICIDE RESISTANT PLANTS**

(57) Abstract: The present invention relates to the production of a non-transgenic plant resistant or tolerant to a herbicide of the phosphonomethylglycine family, e.g., glyphosate. The present invention also relates to the use of a recombinogenic Oligonucleobase to make a desired mutation in the chromosomal or episomal sequences of a plant in the gene encoding for 5-enol pyruvylshikimate-3-phosphate synthase (EPSPS). The mutated protein, which substantially maintains the catalytic activity of the wild-type protein, allows for increased resistance or tolerance of the plant to a herbicide of the phosphonomethylglycine family, and allows for the substantially normal growth or development of the plant, its organs, tissues or cells as compared to the wild-type plant irrespective of the presence or absence of the herbicide. The present invention also relates to a non-transgenic plant cell in which the EPSPS gene has been mutated, a non-transgenic plant regenerated therefrom, as well as a plant resulting from a cross using a regenerated non-transgenic plant having a mutated EPSPS gene.

NON-TRANSGENIC HERBICIDE RESISTANT PLANTS

The present application claims priority to U.S. Provisional Application No. 60/158,027, filed on October 7, 1999 and to U.S. Provisional Application No. 60/173,564, filed December 30, 1999, the disclosures of each of which are incorporated by reference herein in their entirety.

1. FIELD OF THE INVENTION

The present invention relates to the production of a non-transgenic plant resistant or tolerant to a herbicide of the phosphonomethylglycine family, *e.g.*, glyphosate. The present invention also relates to the use of a recombinagenic oligonucleobase to make a desired mutation in the chromosomal or episomal sequences of a plant in the gene encoding for 5-enol pyruvylshikimate-3-phosphate synthase (EPSPS). The mutated protein, which substantially maintains the catalytic activity of the wild-type protein, allows for increased resistance or tolerance of the plant to a herbicide of the phosphonomethylglycine family, and allows for the substantially normal growth or development of the plant, its organs, tissues or cells as compared to the wild-type plant irrespective of the presence or absence of the herbicide. The present invention also relates to a non-transgenic plant cell in which the EPSPS gene has been mutated, a non-transgenic plant regenerated therefrom, as well as a plant resulting from a cross using a regenerated non-transgenic plant having a mutated EPSPS gene.

2. BACKGROUND TO THE INVENTION

2.1 PHOSPHONOMETHYLGLYCINE HERBICIDES

Herbicide-tolerant plants may reduce the need for tillage to control weeds thereby effectively reducing soil erosion. One herbicide which is the subject of much investigation in this regard is N-phosphonomethylglycine, commonly referred to as glyphosate. Glyphosate inhibits the shikimic acid pathway which leads to the biosynthesis of aromatic compounds including amino acids, hormones and vitamins. Specifically, glyphosate curbs the conversion of phosphoenolpyruvic acid (PEP) and 3-phosphoshikimic acid to 5-enolpyruvyl-3-phosphoshikimic acid by inhibiting the enzyme 5-enolpyruvylshikimate-3-phosphate synthase (hereinafter referred to as EPSP synthase or EPSPS). For purposes of the present invention, the term "glyphosate" includes any herbicidally effective form of N-phosphonomethylglycine (including any salt thereof), other forms which result in the production of the glyphosate anion in plants and any other herbicides of the phosphonomethylglycine family.

Tolerance of plants to glyphosate can be increased by introducing a mutant EPSPS gene having an alteration in the EPSPS amino acid coding sequence into the genome of the plant. Examples of some of the mutations in the EPSPS gene for inducing glyphosate tolerance are described in the following patents: U.S. Patent No. 5,310,667; U.S. Patent No. 5,866,775; U.S. Patent No. 5,312,910; U.S. Patent No. 5,145,783. These proposed mutations typically have a higher K_i for glyphosate than the wild-type EPSPS enzyme which confers the glyphosate-tolerant phenotype, but these variants are also characterized by a high K_m for PEP which makes the enzyme kinetically less efficient (Kishore et al., 1988, Ann. Rev. Biochem. 57:627-663; Schulz et al., 1984, Arch. Microbiol. 137: 121-123; Sost et al., 1984, FEBS Lett. 173: 238-241; Kishore et al., 1986, Fed. Proc. 45: 1506; Sost and Amrhein, 1990, Arch. Biochem. Biophys. 282: 433-436). Many mutations of the EPSPS gene are chosen so as to produce an EPSPS enzyme that is resistant to herbicides, but unfortunately, the EPSPS enzyme produced by the mutated EPSPS gene has a significantly lower enzymatic activity than the wild-type EPSPS. For example, the apparent K_m for PEP and the apparent K_i for glyphosate for the wild-type EPSPS from *E. coli* are 10 μ M and 0.5 μ M, while for a glyphosate-tolerant isolate having a single amino acid substitution of alanine for glycine at position 96, these values are 220 μ M and 4.0 mM, respectively. A number of glyphosate-tolerant EPSPS genes have been constructed by mutagenesis. Again, the glyphosate-tolerant EPSPS had lower catalytic efficiency (V_{max}/K_m), as shown by an increase in the K_m for PEP, and a slight reduction of the V_{max} of the wild-type plant enzyme (Kishore et al., 1988, Ann. Rev. Biochem. 57:627-663).

Since the kinetic constants of the variant enzymes are impaired with respect to PEP, it has been proposed that high levels of overproduction of the variant enzyme, 40-80 fold, would be required to maintain normal catalytic activity in plants in the presence of glyphosate (Kishore et al., 1988, Ann. Rev. Biochem. 57:627-663). It has been shown that glyphosate-tolerant plants can be produced by inserting into the genome of the plant the capacity to produce a higher level of EPSP synthase in the chloroplast of the cell (Shah et al., 1986, Science 233, 478-481), which enzyme is preferably glyphosate-tolerant (Kishore et al., 1988, Ann. Rev. Biochem. 57:627-663).

The introduction of the exogenous mutant EPSPS genes into plant is well documented. For example, according to U.S. Patent No. 4,545,060, to increase a plant's resistance to glyphosate, a gene coding for an EPSPS variant having at least one mutation that renders the enzyme more resistant to its competitive inhibitor, *i.e.*, glyphosate, is introduced into the plant genome. However, many complications and problems are associated with these examples. Many such mutations result in low expression of the mutated EPSPS gene product or result in an EPSPS gene product with significantly lower

enzymatic activity as compared to wild type. The low expression or low enzymatic activity of the mutated enzyme results in abnormally low levels of growth and development of the plant.

While such variants in the EPSP synthases have proved useful in obtaining transgenic plants tolerant to glyphosate, it would be increasingly beneficial to obtain a variant EPSPS gene product that is highly glyphosate-tolerant but still kinetically efficient, such that improved tolerance can be obtained with a wild-type expression level.

2.2 RECOMBINAGENIC OLIGONUCLEOBASES

Recombinagenic oligonucleobases and their use to effect genetic changes in eukaryotic cells are described in United States patent No. 5,565,350 to Kmiec (Kmiec I). Kmiec I teaches a method for introducing specific genetic alterations into a target gene. Kmiec I discloses, *inter alia*, recombinagenic oligonucleobases having two strands, in which a first strand contains two segments of at least 8 RNA-like nucleotides that are separated by a third segment of from 4 to about 50 DNA-like nucleotides, termed an "interposed DNA segment." The nucleotides of the first strand are base paired to DNA-like nucleotides of a second strand. The first and second strands are additionally linked by a segment of single stranded nucleotides so that the first and second strands are parts of a single oligonucleotide chain. Kmiec I further teaches a method for introducing specific genetic alterations into a target gene. According to Kmiec I, the sequences of the RNA segments are selected to be homologous, *i.e.*, identical, to the sequence of a first and a second fragment of the target gene. The sequence of the interposed DNA segment is homologous with the sequence of the target gene between the first and second fragment except for a region of difference, termed the "heterologous region." The heterologous region can effect an insertion or deletion, or can contain one or more bases that are mismatched with the sequence of target gene so as to effect a substitution. According to Kmiec I, the sequence of the target gene is altered as directed by the heterologous region, such that the target gene becomes homologous with the sequence of the recombinagenic oligonucleobase. Kmiec I specifically teaches that ribose and 2'-O-methylribose, *i.e.*, 2'-methoxyribose, containing nucleotides can be used in recombinagenic oligonucleobases and that naturally-occurring deoxyribose-containing nucleotides can be used as DNA-like nucleotides.

U.S. Patent No. 5,731,181 to Kmiec (Kmiec II) specifically disclose the use of recombinagenic oligonucleobases to effect genetic changes in plant cells and discloses further examples of analogs and derivatives of RNA-like and DNA-like nucleotides that can be used to effect genetic changes in specific target genes. Other patents discussing the use

of recombinagenic oligonucleobases include: U.S. Patent Nos. 5,756,325; 5,871,984; 5,760,012; 5,888,983; 5,795,972; 5,780,296; 5,945,339; 6,004,804; and 6,010,907 and in International Patent No. PCT/US00/23457; and in International Patent Publication Nos. WO 98/49350; WO 99/07865; WO 99/58723; WO 99/58702; and WO 99/40789.

- 5 Recombinagenic oligonucleobases include mixed duplex oligonucleotides, non-nucleotide containing molecules taught in Kmiec II and other molecules taught in the above-noted patents and patent publications.

Citation or identification of any reference in Section 2, or any section of this application shall not be construed as an admission that such reference is available as prior art to the present invention.

3. SUMMARY OF THE INVENTION

The present invention is directed to a non-transgenic plant or plant cell having one or more mutations in the EPSPS gene, which plant has increased resistance or tolerance to a member of the phosphonomethylglycine family and which plant exhibits substantially normal growth or development of the plant, its organs, tissues or cells, as compared to the corresponding wild-type plant or cell. The present invention is also directed to a non-transgenic plant having a mutation in the EPSPS gene, which plant is resistant to or has an increased tolerance to a member of the phosphonomethylglycine family, *e.g.*, glyphosate, wherein the mutated EPSPS protein has substantially the same catalytic activity as compared to the wild-type EPSPS protein.

The present invention is also directed to a method for producing a non-transgenic plant having a mutated EPSPS gene that substantially maintains the catalytic activity of the wild-type protein irrespective of the presence or absence of a herbicide of the phosphonomethylglycine family. The method comprises introducing into a plant cell a recombinagenic oligonucleobase with a targeted mutation in the EPSPS gene and identifying a cell, seed, or plant having a mutated EPSPS gene.

Illustrative examples of a recombinagenic oligonucleobase is found in following patent publications, which are incorporated in their entirety by reference herein:

30 U.S. Patent Nos. 5,565,350; 5,756,325; 5,871,984; 5,760,012; 5,731,181; 5,888,983; 5,795,972; 5,780,296; 5,945,339; 6,004,804; and 6,010,907 and in International Patent No. PCT/US00/23457; and in International Patent Publication Nos. WO 98/49350; WO 99/07865; WO 99/58723; WO 99/58702; and WO 99/40789.

The plant can be of any species of dicotyledonous, monocotyledonous or gymnospermous plant, including any woody plant species that grows as a tree or shrub, any herbaceous species, or any species that produces edible fruits, seeds or vegetables, or any

species that produces colorful or aromatic flowers. For example, the plant may be selected from a species of plant from the group consisting of canola, sunflower, tobacco, sugar beet, cotton, maize, wheat, barley, rice, sorghum, tomato, mango, peach, apple, pear, strawberry, banana, melon, potato, carrot, lettuce, onion, soya spp, sugar cane, pea, field beans, poplar, grape, citrus, alfalfa, rye, oats, turf and forage grasses, flax, oilseed rape, cucumber, morning glory, balsam, pepper, eggplant, marigold, lotus, cabbage, daisy, carnation, tulip, iris, lily, and nut producing plants insofar as they are not already specifically mentioned.

The recombinagenic oligonucleobase can be introduced into a plant cell using any method commonly used in the art, including but not limited to, microcarriers (biolistic delivery), microfibers, electroporation, microinjection.

The invention is also directed to the culture of cells mutated according to the methods of the present invention in order to obtain a plant that produces seeds, henceforth a "fertile plant", and the production of seeds and additional plants from such a fertile plant.

The invention is further directed to a method of selectively controlling weeds in a field, the field comprising plants with the disclosed EPSPS gene alterations and weeds, the method comprising application to the field of a herbicide to which the said plants have been rendered resistant.

The invention is also directed to novel mutations in the EPSPS gene that confer resistance or tolerance to a member of the phosphonomethylglycine family, *e.g.*, glyphosate, to a plant or wherein the mutated EPSPS has substantially the same enzymatic activity as compared to wild-type EPSPS.

3.1 DEFINITIONS

The invention is to be understood in accordance with the following definitions.

An oligonucleobase is a polymer of nucleobases, which polymer can hybridize by Watson-Crick base pairing to a DNA having the complementary sequence.

Nucleobases comprise a base, which is a purine, pyrimidine, or a derivative or analog thereof. Nucleobases include peptide nucleobases, the subunits of peptide nucleic acids, and morpholine nucleobases as well as nucleosides and nucleotides. Nucleosides are nucleobases that contain a pentosefuranosyl moiety, *e.g.*, an optionally substituted riboside or 2'-deoxyriboside. Nucleosides can be linked by one of several linkage moieties, which may or may not contain a phosphorus. Nucleosides that are linked by unsubstituted phosphodiester linkages are termed nucleotides.

An oligonucleobase chain has a single 5' and 3' terminus, which are the ultimate nucleobases of the polymer. A particular oligonucleobase chain can contain

nucleobases of all types. An oligonucleobase compound is a compound comprising one or more oligonucleobase chains that are complementary and hybridized by Watson-Crick base pairing. Nucleobases are either deoxyribo-type or ribo-type. Ribo-type nucleobases are pentosefuranosyl containing nucleobases wherein the 2' carbon is a methylene substituted
5 with a hydroxyl, alkyloxy or halogen. Deoxyribo-type nucleobases are nucleobases other than ribo-type nucleobases and include all nucleobases that do not contain a pentosefuranosyl moiety.

An oligonucleobase strand generically includes both oligonucleobase chains and segments or regions of oligonucleobase chains. An oligonucleobase strand has a 3' end
10 and a 5' end. When a oligonucleobase strand is coextensive with a chain, the 3' and 5' ends of the strand are also 3' and 5' termini of the chain.

According to the present invention, substantially normal growth of a plant, plant organ, plant tissue or plant cell is defined as a growth rate or rate of cell division of the plant, plant organ, plant tissue, or plant cell that is at least 35%, at least 50%, at least 60%,
15 or at least 75% of the growth rate or rate of cell division in a corresponding plant, plant organ, plant tissue or plant cell expressing the wild type EPSPS protein.

According to the present invention, substantially normal development of a plant, plant organ, plant tissue or plant cell is defined as the occurrence of one or more developmental events in the plant, plant organ, plant tissue or plant cell that are
20 substantially the same as those occurring in a corresponding plant, plant organ, plant tissue or plant cell expressing the wild type EPSPS protein.

According to the present invention plant organs include, but are not limited to, leaves, stems, roots, vegetative buds, floral buds, meristems, embryos, cotyledons, endosperm, sepals, petals, pistils, carpels, stamens, anthers, microspores, pollen, pollen
25 tubes, ovules, ovaries and fruits, or sections, slices or discs taken therefrom. Plant tissues include, but are not limited to, callus tissues, ground tissues, vascular tissues, storage tissues, meristematic tissues, leaf tissues, shoot tissues, root tissues, gall tissues, plant tumor tissues, and reproductive tissues. Plant cells include, but are not limited to, isolated cells with cell walls, variously sized aggregates thereof, and protoplasts.

30 Plants are substantially "tolerant" to glyphosate when they are subjected to it and provide a dose/response curve which is shifted to the right when compared with that provided by similarly subjected non-tolerant like plant. Such dose/response curves have "dose" plotted on the X-axis and "percentage kill", "herbicidal effect", etc., plotted on the y-axis. Tolerant plants will require more herbicide than non-tolerant like plants in order to
35 produce a given herbicidal effect. Plants which are substantially "resistant" to the glyphosate exhibit few, if any, necrotic, lytic, chlorotic or other lesions, when subjected to

glyphosate at concentrations and rates which are typically employed by the agrochemical community to kill weeds in the field. Plants which are resistant to a herbicide are also tolerant of the herbicide. The terms "resistant" and "tolerant" are to be construed as "tolerant and/or resistant" within the context of the present application.

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4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1A is the DNA sequence of *Arabidopsis thaliana* EPSPS gene (SEQ ID NO:1). The bold underlined nucleotide residues are the targeted residues.

FIG. 1B is the amino acid sequence of *Arabidopsis thaliana* EPSPS protein (SEQ ID NO:2). The bold and underlined amino acid residues are the targeted residues.

FIG. 2 is a list of the *Arabidopsis thaliana* wild-type and mutant EPSPS nucleotide and amino acid sequences in the region of amino acid position 173 to 183; wild-type nucleotide sequence (SEQ ID NO:1) and wild-type amino acid sequence (SEQ ID NO:2), mutant A₁₇₇ nucleotide sequence (SEQ ID NO:3) and amino acid sequence (SEQ ID NO:4); mutant I₁₇₈ nucleotide sequence (SEQ ID NO:5) and amino acid sequence (SEQ ID NO:6); mutant A₁₇₇I₁₇₈ nucleotide sequence (SEQ ID NO:7) and amino acid sequence (SEQ ID NO:8); mutant I₁₇₈S₁₈₂ nucleotide sequence (SEQ ID NO:9) and amino acid sequence (SEQ ID NO:10); mutant A₁₇₇S₁₈₂ nucleotide sequence (SEQ ID NO:11) and amino acid sequence (SEQ ID NO:12); mutant A₁₇₇I₁₇₈S₁₈₂ nucleotide sequence (SEQ ID NO:13) and amino acid sequence (SEQ ID NO:14); mutant V₁₇₇S₁₈₂ nucleotide sequence (SEQ ID NO:15) and amino acid sequence (SEQ ID NO:16); mutant L₁₇₈S₁₈₂ nucleotide sequence (SEQ ID NO:17) and amino acid sequence (SEQ ID NO:18); mutant A₁₇₇V₁₇₈ nucleotide sequence (SEQ ID NO:19) and amino acid sequence (SEQ ID NO:20); mutant A₁₇₇L₁₈₂ nucleotide sequence (SEQ ID NO:21) and amino acid sequence (SEQ ID NO:22).

FIG. 3A-C is an alignment of the DNA of *Arabidopsis thaliana* EPSPS gene performed by DNASTar (LaserGene), (SEQ ID NO:1) with the nucleotide sequences of *Brassica napus* (SEQ ID NO:23); *Petunia hybrida* (SEQ ID NO:24); and *Zea mays* (SEQ ID NO:25) EPSPS gene. The sequences are aligned using J. Hein method with weighted residue weight table.

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FIG. 4 is an alignment of the *Arabidopsis thaliana* EPSPS amino acid sequence (SEQ ID NO:2) with the *Brassica napus* (SEQ ID NO:26); *Petunia hybrida* (SEQ ID NO:27); and *Zea mays* (SEQ ID NO:28) EPSPS amino acid sequences. The sequences are aligned using J. Hein method with weighted residue weight table.

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FIG. 5 is a list of the mutagenesis primers used, with the targeted codons in bold characters (mutant primer A₁₇₇ (SEQ ID NO:29); mutant primer I₁₇₈ (SEQ ID NO:30);

mutant primer A₁₇₇I₁₇₈ (SEQ ID NO:31); mutant primer I₁₇₈S₁₈₂ (SEQ ID NO:32); mutant primer A₁₇₇S₁₈₂ (SEQ ID NO:34); mutant primer A₁₇₇I₁₇₈S₁₈₂ (SEQ ID NO:35); mutant primer V₁₇₇S₁₈₂ (SEQ ID NO:35); mutant primer L₁₇₈S₁₈₂ (SEQ ID NO:36); mutant primer A₁₇₇V₁₇₈ (SEQ ID NO:37); and mutant primer A₁₇₇L₁₈₂ (SEQ ID NO:38)).

5 FIG. 6 is the growth measured by optical density at 600 nm of *Arabidopsis* clones in the presence (+) and absence (-) of 17 mM glyphosate.

FIG. 7 (top panel) is a western blot showing the expression of His-tagged *Bacillus*, *Arabidopsis* wild type (WT) and mutant (AS) EPSPS proteins isolated from cell lysates (L) and eluates (E). Untransformed *Salmonella* as a negative control shows no
10 EPSPS expression. The bottom panel is a silver-stained duplicate gel.

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed to a non-transgenic plant or plant cell having a mutation in the EPSPS gene, which plant has increased resistance or tolerance to a
15 member of the phosphonomethylglycine family and which plant exhibits substantially normal growth or development of the plant, its organs, tissues or cells, as compared to the corresponding wild-type plant or cell. The present invention is also directed to a non-transgenic plant having a mutation in the EPSPS gene, which plant is resistant to or has an increased tolerance to a member of the phosphonomethylglycine family, e.g., glyphosate,
20 wherein the mutated EPSPS protein has substantially the same catalytic activity as compared to the wild-type EPSPS protein.

The present invention is also directed to a method for producing a non-transgenic plant having a mutated EPSPS gene that substantially maintains the catalytic activity of the wild-type protein irrespective of the presence or absence of a herbicide of the
25 phosphonomethylglycine family. The method comprises introducing into a plant cell a recombinagenic oligonucleobase with a targeted mutation in the EPSPS gene and identifying a cell, seed, or plant having a mutated EPSPS gene.

Illustrative examples of a recombinagenic oligonucleobase is found in following patent publications, which are incorporated in their entirety by reference herein:
30 U.S. Patent Nos. 5,565,350; 5,756,325; 5,871,984; 5,760,012; 5,731,181; 5,888,983; 5,795,972; 5,780,296; 5,945,339; 6,004,804; and 6,010,907 and in International Patent No. PCT/US00/23457; and in International Patent Publication Nos. WO 98/49350; WO 99/07865; WO 99/58723; WO 99/58702; and WO 99/40789.

The plant can be of any species of dicotyledonous, monocotyledonous or
35 gymnospermous plant, including any woody plant species that grows as a tree or shrub, any herbaceous species, or any species that produces edible fruits, seeds or vegetables, or any

species that produces colorful or aromatic flowers. For example, the plant may be selected from a species of plant from the group consisting of canola, sunflower, tobacco, sugar beet, cotton, maize, wheat, barley, rice, sorghum, tomato, mango, peach, apple, pear, strawberry, banana, melon, potato, carrot, lettuce, onion, soya spp, sugar cane, pea, field beans, poplar, 5 grape, citrus, alfalfa, rye, oats, turf and forage grasses, flax, oilseed rape, cucumber, morning glory, balsam, pepper, eggplant, marigold, lotus, cabbage, daisy, carnation, tulip, iris, lily, and nut producing plants insofar as they are not already specifically mentioned.

The recombinagenic oligonucleobase can be introduced into a plant cell using any method commonly used in the art, including but not limited to, microcarriers 10 (biolistic delivery), microfibers, electroporation, microinjection.

The invention is also directed to the culture of cells mutated according to the methods of the present invention in order to obtain a plant that produces seeds, henceforth a "fertile plant", and the production of seeds and additional plants from such a fertile plant.

The invention is further directed to a method of selectively controlling weeds 15 in a field, the field comprising plants with the disclosed EPSPS gene alterations and weeds, the method comprising application to the field of a herbicide to which the said plants have been rendered resistant.

The invention is also directed to novel mutations in the EPSPS gene that confer resistance or tolerance to a member of the phosphonomethylglycine family, *e.g.*, 20 glyphosate, to a plant or wherein the mutated EPSPS has substantially the same enzymatic activity as compared to wild-type EPSPS.

5.1 RECOMBINAGENIC OLIGONUCLEOBASES

The invention can be practiced with recombinagenic oligonucleobases 25 having the conformations and chemistries described in United States patent No. 5,565,350 to Kmiec (Kmiec I) and U.S. patent No. 5,731,181 (Kmiec II) gene, which are hereby incorporated by reference. Kmiec I teaches a method for introducing specific genetic alterations into a target gene. The recombinagenic oligonucleobases in Kmiec I and/or Kmiec II contain two complementary strands, one of which contains at least one segment of 30 RNA-type nucleotides (an "RNA segment") that are base paired to DNA-type nucleotides of the other strand.

Kmiec II discloses that purine and pyrimidine base-containing non-nucleotides can be substituted for nucleotides. U.S. Patent Nos. 5,756,325; 5,871,984; 5,760,012; 5,888,983; 5,795,972; 5,780,296; 5,945,339; 6,004,804; and 6,010,907 and in 35 International Patent No. PCT/US00/23457; and in International Patent Publication Nos. WO 98/49350; WO 99/07865; WO 99/58723; WO 99/58702; and WO 99/40789, which are each

hereby incorporated in their entirety, disclose additional recombinagenic molecules that can be used for the present invention. The term "recombinagenic oligonucleobase" is used herein to denote the molecules that can be used in the methods of the present invention and include mixed duplex oligonucleotides, non-nucleotide containing molecules taught in Kmiec II, single stranded oligodeoxynucleotides and other recombinagenic molecules taught in the above noted patents and patent publications.

In one embodiment, the recombinagenic oligonucleobase is a mixed duplex oligonucleotide in which the RNA-type nucleotides of the mixed duplex oligonucleotide are made RNase resistant by replacing the 2'-hydroxyl with a fluoro, chloro or bromo functionality or by placing a substituent on the 2'-O. Suitable substituents include the substituents taught by the Kmiec II. Alternative substituents include the substituents taught by U.S. Patent No. 5,334,711 (Sproat) and the substituents taught by patent publications EP 629 387 and EP 679 657 (collectively, the Martin Applications), which are hereby incorporated by reference. As used herein, a 2' -fluoro, chloro or bromo derivative of a ribonucleotide or a ribonucleotide having a 2'-OH substituted with a substituent described in the Martin Applications or Sproat is termed a "2'-Substituted Ribonucleotide." As used herein the term "RNA-type nucleotide" means a 2'-hydroxyl or 2'-Substituted Nucleotide that is linked to other nucleotides of a mixed duplex oligonucleotide by an unsubstituted phosphodiester linkage or any of the non-natural linkages taught by Kmiec I or Kmiec II. As used herein the term "deoxyribo-type nucleotide" means a nucleotide having a 2'-H, which can be linked to other nucleotides of a MDON by an unsubstituted phosphodiester linkage or any of the non-natural linkages taught by Kmiec I or Kmiec II.

In a particular embodiment of the present invention, the recombinagenic oligonucleobase is a mixed duplex oligonucleotide that is linked solely by unsubstituted phosphodiester bonds. In alternative embodiments, the linkage is by substituted phosphodiester, phosphodiester derivatives and non-phosphorus-based linkages as taught by Kmiec II. In yet another embodiment, each RNA-type nucleotide in the mixed duplex oligonucleotide is a 2'-Substituted Nucleotide. Particular preferred embodiments of 2'-Substituted Ribonucleotides are 2'-fluoro, 2'-methoxy, 2'-propyloxy, 2'-allyloxy, 2'-hydroxyethyloxy, 2'-methoxyethyloxy, 2'-fluoropropyloxy and 2'-trifluoropropyloxy substituted ribonucleotides. More preferred embodiments of 2'-Substituted Ribonucleotides are 2'-fluoro, 2'-methoxy, 2'-methoxyethyloxy, and 2'-allyloxy substituted nucleotides. In another embodiment the mixed duplex oligonucleotide is linked by unsubstituted phosphodiester bonds.

Although mixed duplex oligonucleotide having only a single type of 2'-substituted RNA-type nucleotide are more conveniently synthesized, the methods of the

invention can be practiced with mixed duplex oligonucleotides having two or more types of RNA-type nucleotides. The function of an RNA segment may not be affected by an interruption caused by the introduction of a deoxynucleotide between two RNA-type trinucleotides, accordingly, the term RNA segment encompasses such an "interrupted RNA segment." An uninterrupted RNA segment is termed a contiguous RNA segment. In an alternative embodiment an RNA segment can contain alternating RNase-resistant and unsubstituted 2'-OH nucleotides. The mixed duplex oligonucleotides preferably have fewer than 100 nucleotides and more preferably fewer than 85 nucleotides, but more than 50 nucleotides. The first and second strands are Watson-Crick base paired. In one embodiment the strands of the mixed duplex oligonucleotide are covalently bonded by a linker, such as a single stranded hexa, penta or tetranucleotide so that the first and second strands are segments of a single oligonucleotide chain having a single 3' and a single 5' end. The 3' and 5' ends can be protected by the addition of a "hairpin cap" whereby the 3' and 5' terminal nucleotides are Watson-Crick paired to adjacent nucleotides. A second hairpin cap can, additionally, be placed at the junction between the first and second strands distant from the 3' and 5' ends, so that the Watson-Crick pairing between the first and second strands is stabilized.

The first and second strands contain two regions that are homologous with two fragments of the target EPSPS gene, *i.e.*, have the same sequence as the target gene. A homologous region contains the nucleotides of an RNA segment and may contain one or more DNA-type nucleotides of connecting DNA segment and may also contain DNA-type nucleotides that are not within the intervening DNA segment. The two regions of homology are separated by, and each is adjacent to, a region having a sequence that differs from the sequence of the target gene, termed a "heterologous region." The heterologous region can contain one, two or three mismatched nucleotides. The mismatched nucleotides can be contiguous or alternatively can be separated by one or two nucleotides that are homologous with the target gene. Alternatively, the heterologous region can also contain an insertion or one, two, three or of five or fewer nucleotides. Alternatively, the sequence of the mixed duplex oligonucleotide may differ from the sequence of the target gene only by the deletion of one, two, three, or five or fewer nucleotides from the mixed duplex oligonucleotide. The length and position of the heterologous region is, in this case, deemed to be the length of the deletion, even though no nucleotides of the mixed duplex oligonucleotide are within the heterologous region. The distance between the fragments of the target gene that are complementary to the two homologous regions is identically the length of the heterologous region when a substitution or substitutions is intended. When the heterologous region contains an insertion, the homologous regions are thereby separated in

the mixed duplex oligonucleotide farther than their complementary homologous fragments are in the gene, and the converse is applicable when the heterologous region encodes a deletion.

The RNA segments of the mixed duplex oligonucleotides are each a part of a
5 homologous region, *i.e.*, a region that is identical in sequence to a fragment of the target gene, which segments together preferably contain at least 13 RNA-type nucleotides and preferably from 16 to 25 RNA-type nucleotides or yet more preferably 18-22 RNA-type nucleotides or most preferably 20 nucleotides. In one embodiment, RNA segments of the
10 DNA segment. In one embodiment, each nucleotide of the heterologous region is a nucleotide of the intervening DNA segment. An intervening DNA segment that contains the heterologous region of a mixed duplex oligonucleotide is termed a "mutator segment."

The change to be introduced into the target EPSPS gene is encoded by the heterologous region. The change to be introduced into the EPSPS gene may be a change in
15 one or more bases of the EPSPS gene sequence or the addition or deletion of one or more bases.

In another embodiment of the present invention, the recombinagenic oligonucleobase is a single stranded oligodeoxynucleotide mutational vector or SSOMV, which is disclosed in International Patent Application PCT/US00/23457, which is
20 incorporated by reference in its entirety. The sequence of the SSOMV is based on the same principles as the mutational vectors described in U.S. Patent Nos. 5,756,325; 5,871,984; 5,760,012; 5,888,983; 5,795,972; 5,780,296; 5,945,339; 6,004,804; and 6,010,907 and in International Publication Nos. WO 98/49350; WO 99/07865; WO 99/58723; WO 99/58702; and WO 99/40789. The sequence of the SSOMV contains two regions that are homologous
25 with the target sequence separated by a region that contains the desired genetic alteration termed the mutator region. The mutator region can have a sequence that is the same length as the sequence that separates the homologous regions in the target sequence, but having a different sequence. Such a mutator region can cause a substitution. Alternatively, the homologous regions in the SSOMV can be contiguous to each other, while the regions in the
30 target gene having the same sequence are separated by one, two or more nucleotides. Such a SSOMV causes a deletion from the target gene of the nucleotides that are absent from the SSOMV. Lastly, the sequence of the target gene that is identical to the homologous regions may be adjacent in the target gene but separated by one two or more nucleotides in the sequence of the SSOMV. Such an SSOMV causes an insertion in the sequence of target
35 gene.

The nucleotides of the SSOMV are deoxyribonucleotides that are linked by unmodified phosphodiester bonds except that the 3' terminal and/or 5' terminal internucleotide linkage or alternatively the two 3' terminal and/or 5' terminal internucleotide linkages can be a phosphorothioate or phosphoamidate. As used herein an internucleotide linkage is the linkage between nucleotides of the SSOMV and does not include the linkage between the 3' end nucleotide or 5' end nucleotide and a blocking substituent, see *supra*. In a specific embodiment the length of the SSOMV is between 21 and 55 deoxynucleotides and the lengths of the homology regions are, accordingly, a total length of at least 20 deoxynucleotides and at least two homology regions should each have lengths of at least 8 deoxynucleotides.

The SSOMV can be designed to be complementary to either the coding or the non-coding strand of the target gene. When the desired mutation is a substitution of a single base, it is preferred that both the mutator nucleotide be a pyrimidine. To the extent that is consistent with achieving the desired functional result it is preferred that both the mutator nucleotide and the targeted nucleotide in the complementary strand be pyrimidines. Particularly preferred are SSOMV that encode transversion mutations, *i.e.*, a C or T mutator nucleotide is mismatched, respectively, with a C or T nucleotide in the complementary strand.

In addition to the oligodeoxynucleotide the SSOMV can contain a 5' blocking substituent that is attached to the 5' terminal carbons through a linker. The chemistry of the linker is not critical other than its length, which should preferably be at least 6 atoms long and that the linker should be flexible. A variety of non-toxic substituents such as biotin, cholesterol or other steroids or a non-intercalating cationic fluorescent dye can be used. Particularly preferred as reagents to make SSOMV are the reagents sold as Cy3TM and Cy5TM by Glen Research, Sterling VA, which are blocked phosphoroamidites that upon incorporation into an oligonucleotide yield 3,3,3',3'-tetramethyl N,N'-isopropyl substituted indomonocarbocyanine and indodicarbocyanine dyes, respectively. Cy3 is the most preferred. When the indocarbocyanine is N-oxyalkyl substituted it can be conveniently linked to the 5' terminal of the oligodeoxynucleotide through as a phosphodiester with a 5' terminal phosphate. The chemistry of the dye linker between the dye and the oligodeoxynucleotide is not critical and is chosen for synthetic convenience.

When the commercially available Cy3 phosphoramidite is used as directed the resulting 5' modification consists of a blocking substituent and linker together which are a N-hydroxypropyl, N'-phosphatidylpropyl 3,3,3',3'-tetramethyl indomonocarbocyanine.

In the preferred embodiment the indocarbocyanine dye is tetra substituted at the 3 and 3' positions of the indole rings. Without limitation as to theory these substitutions

prevent the dye from being an intercalating dye. The identity of the substituents at these positions are not critical. The SSOMV can in addition have a 3' blocking substituent. Again the chemistry of the 3' blocking substituent is not critical.

5 5.2 THE LOCATION AND TYPE OF MUTATION INTRODUCED INTO THE EPSPS GENE

In one embodiment of the present invention, the *Arabidopsis thaliana* EPSPS gene (see Figure 1A) and corresponding EPSPS enzyme (see Figure 1B) comprises a mutation at one or more amino acid residues selected from the group consisting of Leu₁₇₃,
10 Gly₁₇₇, Thr₁₇₈, Ala₁₇₉, Met₁₈₀, Arg₁₈₁, Pro₁₈₂, Ser₉₈, Ser₂₅₅ and Leu₁₉₈, or at an analogous position in an EPSPS paralog, and the mutation results in one or more of the following amino acid substitutions in the EPSPS enzyme in comparison with the wild-type sequence:

- (i) Leu₁₇₃ - Phe
- (ii) Gly₁₇₇ - Ala or Ile
- 15 (iii) Thr₁₇₈ - Ile or Val or Leu
- (iv) Ala₁₇₉ - Gly
- (v) Met₁₈₀ - Cys
- (vi) Arg₁₈₁ - Leu or Ser
- (vii) Pro₁₈₂ - Leu or Ser
- 20 (viii) Ser₉₈ - Asp
- (ix) Ser₂₅₅ - Ala
- (x) Leu₁₉₈ - Lys.

In another embodiment of the present invention, within the EPSPS gene product, the amino acid residue to be changed is Leu within the contiguous sequence Leu-
25 Tyr-Leu-Gly-Asn (SEQ ID NO:29) and is changed to Phe; or the amino acid residue to be changed is Gly within the contiguous sequence Asn-Ala-Gly-Thr-Ala (SEQ ID NO:30) and is changed to Ala or Ile; or the amino acid to be changed is Thr within the contiguous sequence Ala-Gly-Thr-Ala-Met (SEQ ID NO:31) and is changed to Ile, Val or Leu; or the amino acid to be changed is Ala within the contiguous sequence Gly-Thr-Ala-Met-Arg
30 (SEQ ID NO:32) and is changed to Gly; or the amino acid to be changed is Met within the contiguous sequence Thr-Ala-Met-Arg-Pro (SEQ ID NO:33) and is changed to Cys; or the amino acid to be changed is Arg within the contiguous sequence Ala-Met-Arg-Pro-Leu (SEQ ID NO:34) and is changed to Leu or Ser; or the amino acid to be changed is Pro within the contiguous sequence Met-Arg-Pro-Leu-Thr (SEQ ID NO:35) and is changed to
35 Leu or Ser; or the amino acid to be changed is Ser within a contiguous Pro-Gly-Ser-Lys-Ser (SEQ ID NO:36) and is changed to Asp; or the amino acid to be changed is Ser within the

contiguous sequence Ile-Ser-Ser-Gln-Tyr (SEQ ID NO:37) and is changed to Ala; or the amino acid to be changed is Leu within the contiguous sequence Tyr-Val-Leu-Asp-Gly (SEQ ID NO:38) and is changed to Lys. In other embodiments, one or more of the foregoing changes can be made in the EPSPS amino acid sequence.

5 Alternatively, and/or additionally, the mutation may result in the replacement of any amino acid at positions corresponding to 256, 284-288 and 353-356 with respect to the EPSPS protein depicted in Figure 1B (SEQ ID NO. 2).

In specific embodiments of the present invention, the EPSPS gene is mutated at amino acid position 177 in which Gly is replaced by Ala. Another specific embodiment
10 is the substitution of Thr at amino acid position 178 by Ile. A further specific embodiment comprises a mutation at amino acid position 177 in which Gly is replaced by Ala, plus the additional substitution of Thr at amino acid position 178 by Ile. Other specific embodiments of the present invention are directed to mutations at amino acid position 178, in which Thr is replaced by Ile, plus the additional mutation at position 182, in which Pro is
15 replaced by Ser. Other embodiments include the substitution of Gly at amino acid position 177 by Ala, plus the additional mutation at amino acid position 182, in which Pro is substituted by Ser. Other mutated EPSPS sequences comprise the substitution of Gly at position 177 by Ala, plus the substitution at position 178, in which Thr is replaced by Ile, plus the additional substitution of Pro at amino acid position 182 by Ser. Another
20 embodiment is the substitution of Thr at amino acid position 178 by Val and the additional mutation at amino acid position 182, in which Pro is replaced by Ser. A further specific embodiment includes the substitution of Thr at position 178 by Leu, plus the mutation at amino acid position 182, in which Pro is replaced by Ser. A further embodiment includes, the substitution at amino acid position 177 in which Gly is replaced by Ala, plus the
25 substitution of Thr at position 178 by Val. The invention also embodies the substitution at amino acid position 177 in which Gly is replaced by Ala, plus the replacement of Thr at amino acid position 178 by Leu (see Figure 2).

The foregoing mutations in the EPSPS gene were described using the *Arabidopsis thaliana* EPSPS gene (SEQ ID NO:1) and protein (SEQ ID NO:2). The
30 present invention also encompasses mutant EPSPS genes of other species (paralogs). However, due to variations in the EPSPS genes of different species, the number of the amino acid residue to be changed in one species may be different in another species.

Nevertheless, the analogous position is readily identified by one of skill in the art by sequence homology. For example, Figure 3A-C shows the aligned nucleotide sequences
35 and Figure 4 shows the aligned amino acid sequences of four paralogs of the EPSPS gene, *Arabidopsis thaliana*, *Zea mays*, *Petunia hybrida*, and *Brassica napus*. Thus, the analogous

positions in *Zea mays* are Leu₉₇, Gly₁₀₁, Thr₁₀₂, Ala₁₀₃, Met₁₀₄, Arg₁₀₅, Pro₁₀₆, Ser₂₃, Ser₁₇₉ and Leu₁₂₂. Thus, the *Zea mays* EPSPS amino acid sequence is mutated at one or more of the following amino acid positions and results in one or more of the following substitutions:

- (i) Leu₉₇ - Phe
- 5 (ii) Gly₁₀₁ - Ala or Ile
- (iii) Thr₁₀₂ - Ile or Val or Leu
- (iv) Ala₁₀₃ - Gly
- (v) Met₁₀₄ - Cys
- (vi) Arg₁₀₅ - Leu or Ser
- 10 (vii) Pro₁₀₆ - Leu or Ser
- (viii) Ser₂₃ -Asp
- (ix) Ser₁₇₉ -Ala
- (x) Leu₁₂₂ -Lys.

In another embodiment of the present invention, within the *Zea mays* EPSPS gene product the amino acid residue to be changed is Leu within the contiguous sequence Leu-Phe-Leu-Gly-Asn (SEQ ID NO:39) and is changed to Phe; or the amino acid residue to be changed is Gly within the contiguous sequence Asn-Ala-Gly-Thr-Ala (SEQ ID NO:30) and is changed to Ala or Ile; or the amino acid to be changed is Thr within the contiguous sequence Ala-Gly-Thr-Ala-Met (SEQ ID NO:31) and is changed to Ile, Val or Leu; or the amino acid to be changed is Ala within the contiguous sequence Gly-Thr-Ala-Met-Arg (SEQ ID NO:32) and is changed to Gly; or the amino acid to be changed is Met within the contiguous sequence Thr-Ala-Met-Arg-Pro (SEQ ID NO:33) and is changed to Cys; or the amino acid to be changed is Arg within the contiguous sequence Ala-Met-Arg-Pro-Leu (SEQ ID NO:34) and is changed to Leu or Ser; or the amino acid to be changed is Pro within the contiguous sequence Met-Arg-Pro-Leu-Thr (SEQ ID NO:35) and is changed to Leu or Ser; or the amino acid to be changed is Ser within a contiguous Pro-Gly-Ser-Lys-Ser (SEQ ID NO:36) and is changed to Asp; or the amino acid to be changed is Ser within the contiguous sequence Ile-Ser-Ser-Gln-Tyr (SEQ ID NO:37) and is changed to Ala; or the amino acid to be changed is Leu within the contiguous sequence Tyr-Val-Leu-Asp-Gly (SEQ ID NO:38) and is changed to Lys. In other embodiments, one or more of the foregoing changes can be made in the EPSPS amino acid sequence.

In *Brassica napus*, the analogous amino acid positions are Leu₁₆₉, Gly₁₇₃, Thr₁₇₄, Ala₁₇₅, Met₁₇₆, Arg₁₇₇, Pro₁₇₈, Ser₉₄, Ser₂₅₁ and Leu₁₉₄. Thus, the *Brassica napus* EPSPS amino acid sequence is mutated at one or more of the following amino acid positions and results in one or more of the following substitutions:

- (i) Leu₁₆₉ - Phe

- (ii) Gly₁₇₃ - Ala or Ile
- (iii) Thr₁₇₄ - Ile or Val or Leu
- (iv) Ala₁₇₅ - Gly
- (v) Met₁₇₆ - Cys
- 5 (vi) Arg₁₇₇ - Leu or Ser
- (vii) Pro₁₇₈ - Leu or Ser
- (viii) Ser₉₄ - Asp
- (ix) Ser₂₅₁ - Ala
- (x) Leu₁₉₄ - Lys

10 In another embodiment of the present invention, within the *Brassica napus* EPSPS gene product the amino acid residue to be changed is Leu within the contiguous sequence Leu-Tyr-Leu-Gly-Asn (SEQ ID NO:29) and is changed to Phe; or the amino acid residue to be changed is Gly within the contiguous sequence Asn-Ala-Gly-Thr-Ala (SEQ ID NO:30) and is changed to Ala or Ile; or the amino acid to be changed is Thr within the

15 contiguous sequence Ala-Gly-Thr-Ala-Met (SEQ ID NO:31) and is changed to Ile, Val or Leu; or the amino acid to be changed is Ala within the contiguous sequence Gly-Thr-Ala-Met-Arg (SEQ ID NO:32) and is changed to Gly; or the amino acid to be changed is Met within the contiguous sequence Thr-Ala-Met-Arg-Pro (SEQ ID NO:33) and is changed to Cys; or the amino acid to be changed is Arg within the contiguous sequence Ala-Met-Arg-

20 Pro-Leu (SEQ ID NO:34) and is changed to Leu or Ser; or the amino acid to be changed is Pro within the contiguous sequence Met-Arg-Pro-Leu-Thr (SEQ ID NO:35) and is changed to Leu or Ser; or the amino acid to be changed is Ser within a contiguous Pro-Gly-Ser-Lys-Ser (SEQ ID NO:36) and is changed to Asp; or the amino acid to be changed is Ser within the contiguous sequence Ile-Ser-Ser-Gln-Tyr (SEQ ID NO:37) and is changed to Ala; or the

25 amino acid to be changed is Leu within the contiguous sequence Tyr-Val-Leu-Asp-Gly (SEQ ID NO:38) and is changed to Lys. In other embodiments, one or more of the foregoing changes can be made in the EPSPS amino acid sequence.

In *Petunia hybrida* the analogous positions are Leu₁₆₉, Gly₁₇₃, Thr₁₇₄, Ala₁₇₅, Met₁₇₆, Arg₁₇₇, Pro₁₇₈, Ser₉₄, Ser₂₅₁ and Leu₁₉₄. Thus, the *Petunia hybrida* EPSPS amino acid

30 sequence is mutated at one or more of the following amino acid positions and results in one or more of the following substitutions:

-
- (i) Leu₁₆₉ - Phe
 - (ii) Gly₁₇₃ - Ala or Ile
 - (iii) Thr₁₇₄ - Ile or Val or Leu
 - 35 (iv) Ala₁₇₅ - Gly
 - (v) Met₁₇₆ - Cys

- (vi) Arg₁₇₇ - Leu or Ser
- (vii) Pro₁₇₈ - Leu or Ser
- (viii) Ser₉₄ -Asp
- (ix) Ser₂₅₁ -Ala
- 5 (x) Leu₁₉₄ -Lys

In another embodiment of the present invention, within the *Petunia hybrida* EPSPS gene product the amino acid residue to be changed is Leu within the contiguous sequence Leu-Phe-Leu-Gly-Asn (SEQ ID NO:39) and is changed to Phe; or the amino acid residue to be changed is Gly within the contiguous sequence Asn-Ala-Gly-Thr-Ala (SEQ ID NO:30) and is changed to Ala or Ile; or the amino acid to be changed is Thr within the contiguous sequence Ala-Gly-Thr-Ala-Met (SEQ ID NO:31) and is changed to Ile, Val or Leu; or the amino acid to be changed is Ala within the contiguous sequence Gly-Thr-Ala-Met-Arg (SEQ ID NO:32) and is changed to Gly; or the amino acid to be changed is Met within the contiguous sequence Thr-Ala-Met-Arg-Pro (SEQ ID NO:33) and is changed to Cys; or the amino acid to be changed is Arg within the contiguous sequence Ala-Met-Arg-Pro-Leu (SEQ ID NO:34) and is changed to Leu or Ser; or the amino acid to be changed is Pro within the contiguous sequence Met-Arg-Pro-Leu-Thr (SEQ ID NO:35) and is changed to Leu or Ser; or the amino acid to be changed is Ser within a contiguous Pro-Gly-Ser-Lys-Ser (SEQ ID NO:36) and is changed to Asp; or the amino acid to be changed is Ser within 15 the contiguous sequence Ile-Ser-Ser-Gln-Tyr (SEQ ID NO:37) and is changed to Ala; or the amino acid to be changed is Leu within the contiguous sequence Tyr-Val-Leu-Asp-Gly (SEQ ID NO:38) and is changed to Lys. In other embodiments, one or more of the foregoing changes can be made in the EPSPS amino acid sequence.

25 5.3 THE DELIVERY OF RECOMBINAGENIC OLIGONUCLEOBASES INTO PLANT CELLS

Any commonly known method can be used in the methods of the present invention to transform a plant cell with a recombinagenic oligonucleobases. Illustrative methods are listed below.

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5.3.1 MICROCARRIERS AND MICROFIBERS

The use of metallic microcarriers (microspheres) for introducing large fragments of DNA into plant cells having cellulose cell walls by projectile penetration is well known to those skilled in the relevant art (henceforth biolistic delivery). United States 35 Patent Nos. 4,945,050; 5,100,792 and 5,204,253 describe general techniques for selecting microcarriers and devices for projecting them.

Specific conditions for using microcarriers in the methods of the present invention are described in International Publication WO 99/07865. In an illustrative technique, ice cold microcarriers (60 mg/ml), mixed duplex oligonucleotide (60 mg/ml) 2.5 M CaCl_2 and 0.1 M spermidine are added in that order; the mixture gently agitated, *e.g.*, by vortexing, for 10 minutes and let stand at room temperature for 10 minutes, whereupon the microcarriers are diluted in 5 volumes of ethanol, centrifuged and resuspended in 100% ethanol. Good results can be obtained with a concentration in the adhering solution of 8-10 $\mu\text{g}/\mu\text{l}$ microcarriers, 14-17 $\mu\text{g}/\text{ml}$ mixed duplex oligonucleotide, 1.1-1.4 M CaCl_2 and 18-22 mM spermidine. Optimal results were observed under the conditions of 8 $\mu\text{g}/\mu\text{l}$ microcarriers, 16.5 $\mu\text{g}/\text{ml}$ mixed duplex oligonucleotide, 1.3 M CaCl_2 and 21 mM spermidine.

Recombinagenic oligonucleobases can also be introduced into plant cells for the practice of the present invention using microfibers to penetrate the cell wall and cell membrane. U.S. Patent No. 5,302,523 to Coffee et al. describes the use of 30 x 0.5 μm and 10 x 0.3 μm silicon carbide fibers to facilitate transformation of suspension maize cultures of Black Mexican Sweet. Any mechanical technique that can be used to introduce DNA for transformation of a plant cell using microfibers can be used to deliver recombinagenic oligonucleobases for transmutation.

An illustrative technique for microfiber delivery of a recombinagenic oligonucleobase is as follows: Sterile microfibers (2 μg) are suspended in 150 μl of plant culture medium containing about 10 μg of a mixed duplex oligonucleotide. A suspension culture is allowed to settle and equal volumes of packed cells and the sterile fiber/nucleotide suspension are vortexed for 10 minutes and plated. Selective media are applied immediately or with a delay of up to about 120 hours as is appropriate for the particular trait.

5.3.2 PROTOPLAST ELECTROPORATION

In an alternative embodiment, the recombinagenic oligonucleobases can be delivered to the plant cell by electroporation of a protoplast derived from a plant part. The protoplasts are formed by enzymatic treatment of a plant part, particularly a leaf, according to techniques well known to those skilled in the art. *See, e.g.*, Gallois et al., 1996, in *Methods in Molecular Biology* 55:89-107, Humana Press, Totowa, NJ; Kipp et al., 1999, in *Methods in Molecular Biology* 133:213-221, Humana Press, Totowa, NJ. The protoplasts need not be cultured in growth media prior to electroporation. Illustrative conditions for electroporation are 3×10^5 protoplasts in a total volume of 0.3 ml with a concentration of recombinagenic oligonucleobase of between 0.6 - 4 $\mu\text{g}/\text{mL}$.

5.3.3 WHISKERS AND MICROINJECTION

In yet another alternative embodiment, the recombinagenic oligonucleobase can be delivered to the plant cell by whiskers or microinjection of the plant cell. The so called whiskers technique is performed essentially as described in Frame et al., 1994, Plant J. 6:941-948. The recombinagenic oligonucleobase is added to the whiskers and used to transform the plant cells. The recombinagenic oligonucleobase may be co-incubated with plasmids comprising sequences encoding proteins capable of forming recombinase complexes in plant cells such that recombination is catalyzed between the oligonucleotide and the target sequence in the EPSPS gene.

10

5.4 SELECTION OF GLYPHOSATE RESISTANT PLANTS

Plants or plant cells can be tested for resistance or tolerance to a herbicide using commonly known methods in the art, e.g., by growing the plant or plant cell in the presence of a herbicide and measuring the rate of growth as compared to the growth rate in the absence of the herbicide.

15

6. EXAMPLE

The following experiments demonstrate the production of mutant *Arabidopsis thaliana* EPSPS genes which are resistant to the herbicide glyphosate and which allows the plant cells to maintain a growth rate

20

6.1 MATERIAL AND METHODS

6.1.1 ISOLATION OF ARABIDOPSIS THALIANA EPSPS cDNA

A 1.3 kb DNA fragment was amplified by PCR from an *Arabidopsis* cDNA library using the primers AtEXPEXPM1 and AtEXPEXP2CM-2. The two primers were designed to amplify the cDNA from the mature peptide to the termination codon. The 5' primer AtEXPEXPM1 contains an XbaI site (underlined) and the 3' primer AtEXPEXP2CM-2 contains a BglII site (underlined), sites which will be of use for cloning of the fragment into the expression vector.

30

AtEXPEXPM1

5'-GCTCTAGAGAAAGCGTCGGAGATTGTACTT-3' (SEQ ID NO:40)

AtEXPEXP2CM-2

35 5'-GCAGATCTGAGCTCTTAGTGCTTTGTGATTCTTTCAAGTAC-3' (SEQ ID NO:41)

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flanking primer (5'ATEPS-198: 5'- GAAAGCGTCGGAGATTGTAC-3' (SEQ ID NO:44)) and one of the mutation-carrying primers (see Figure 5).

The 353bp PCR fragments obtained were purified (Qiagen PCR Purification kit) and their sequence confirmed. The fragments were then digested with PstI (underlined in the primer sequences) and BamHI and ligated to the pAtEPS-12 vector, which had itself been previously digested with PstI and BamHI. JM109 (Promega) competent cells were used for the transformation and plated onto chloramphenicol-containing LB plates. Clones from each mutagenesis experiment were then isolated and their sequence confirmed.

6.1.5 GLYPHOSATE RESISTANCE ASSAYS

Electrocompetent cells of SA4247, a LacZ - *Salmonella typhi* strain, were prepared according to well known procedures (see Current Protocols in Molecular Biology, (Wiley and Sons, Inc.)). 30 μ l of SA4247 competent cells were electroporated with 20 ng of each plasmid DNA encoding *Arabidopsis* wild-type and mutant EPSPS proteins, *Bacillus* wild-type EPSPS, along with a mock transfection as a control. The settings for electroporation were 25 μ F, 2.5KV and 200 ohms. After electroporation, the cells were transferred into 15 mls culture tube and supplemented with 970 μ l of SOC medium. The cultures were incubated for 1 ½ hours at 37°C at 225 rpm. 50 μ l of each culture were plated onto LB plates containing 17 μ g/ml chloramphenicol (in duplicates) and incubated overnight at 37°C. On the following day, 5 colonies of each plate were picked and transferred onto M9 plates and incubated overnight at 37°C.

Colonies from the overnight incubation on solid M9 were inoculated into 4 ml of liquid M9 medium and grown overnight at 37°C. On the following day, 25 ml of liquid M9 medium containing chloramphenicol, IPTG and 17 mM or 0 mM Glyphosate (Aldrich, 33775-7) were inoculated with 1-2 mls of each overnight culture (in duplicates), the starting OD (at 600 nm) was measured and all the cultures were normalized to start at the same OD. An OD measurement was taken every hour for seven hours. As a control of the bacterial growth, a culture of untransformed *Salmonella* was also inoculated into plain LB medium. In two independent experiments, the clones A₁₇₇I₁₇₈, A₁₇₇V₁₇₈, A₁₇₇L₁₇₈ and I₁₇₇ did not grow in M9 medium, therefore the glyphosate-resistance assays could not be performed on them.

6.1.7 ISOLATION AND PURIFICATION OF THE EXPRESSED PROTEIN FROM BACTERIAL CLONES

One milliliter of overnight culture of each of the bacterial clones is inoculated into 100 ml of liquid LB medium containing chloramphenicol. The cells were

allowed to grow at 37°C until they reached an OD of 0.5-0.7 (approximately 3 ½ hours). IPTG was then added to the cultures to a concentration of 1.0 mM. The cells were grown five additional hours. They were then pelleted at 4000 rpm for 20 minutes at 4°C.

The isolation and the purification of the His-tagged proteins were performed following the Qiagen Ni-NTA Protein Purification System. Cell lysates and eluates were run in duplicates on 12.5% acrylamide gels. One of the gels was silver-stained for immediate visualization, the second gel was transferred onto Millipore Immobilon-P membrane, and blocked overnight in 5% milk in TBS-T. The membrane was then exposed to Anti-His primary antibody solution (Amersham Pharmacia biotech, cat# 37-4710), followed by exposure to Anti-Mouse-IgG secondary antibody solution. (NIF825, from Amersham Pharmacia biotech ECL Western blotting analysis system, cat# RPN2108). Washes and detection reactions were performed according to the manufacturer instructions. Autoradiograms were developed after 5 minutes exposure.

6.2 RESULTS

Cells containing a mutation in the EPSPS gene produced cells that were both resistant to the herbicide glyphosate and that had a substantially similar growth rate in the absence or presence of glyphosate, as compared to the wild-type cells, irrespective of the presence of glyphosate (see Figure 6).

It was also demonstrated that the *Arabidopsis* clones containing a mutant EPSPS gene expressed the mutant protein at substantially the same level as the wild-type protein (see Figure 7).

The invention claimed and described herein is not to be limited in scope by the specific embodiments, including but not limited to the deposited microorganism embodiments, herein disclosed since these embodiments are intended as illustrations of several aspects of the invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims.

A number of references are cited herein, the entire disclosures of which are incorporated herein, in their entirety, by reference.

WE CLAIM:

1. A non-transgenic herbicide resistant plant, which plant expresses a mutant EPSPS gene product and which plant has substantially normal growth as compared to a
5 plant expressing the wild-type EPSPS gene product.
2. A non-transgenic herbicide resistant plant, which plant expresses a mutant EPSPS gene product, which gene product has substantially the same level of catalytic activity as compared to the wild-type gene product.
- 10 3. The plant according to claim 1 or 2 in which the herbicide is a member of the phosphonomethylglycine family.
4. The plant according to claim 3 in which the member of the
15 phosphonomethylglycine family is glyphosate.
5. The plant according to claim 1 or 2 in which the EPSPS gene is mutated at one or more amino acid positions, said positions selected from the group consisting of Leu₁₇₃, Gly₁₇₇, Thr₁₇₈, Ala₁₇₉, Met₁₈₀, Arg₁₈₁, Pro₁₈₂, Ser₉₈, Ser₂₅₅ and Leu₁₉₈ in *Arabidopsis* or
20 at an analogous amino acid residue in an EPSPS paralog.
6. The plant according to claim 5 in which the positions in the *Zea mays* paralog are selected from the group consisting of Leu₉₇, Gly₁₀₁, Thr₁₀₂, Ala₁₀₃, Met₁₀₄, Arg₁₀₅, Pro₁₀₆, Ser₂₃, Ser₁₇₉ and Leu₁₂₂.
- 25 7. The plant according to claim 5 in which the positions in the *Brassica napus* paralog are selected from the group consisting of Leu₁₆₉, Gly₁₇₃, Thr₁₇₄, Ala₁₇₅, Met₁₇₆, Arg₁₇₇, Pro₁₇₈, Ser₉₄, Ser₂₅₁ and Leu₁₉₄.
- 30 8. The plant according to claim 5 in which the positions in the *Petunia hybrida* are selected from the group consisting of Leu₁₆₉, Gly₁₇₃, Thr₁₇₄, Ala₁₇₅, Met₁₇₆, Arg₁₇₇, Pro₁₇₈, Ser₉₄, Ser₂₅₁ and Leu₁₉₄.
9. The plant according to claim 1 or 2 in which the plant is selected from the
35 group consisting of corn, wheat, rice, barley, soybean, cotton, sugarbeet, oilseed rape,

canola, flax, sunflower, potato, tobacco, tomato, alfalfa, poplar, pine, eukalyptus, apple, lettuce, peas, lentils, grape and turf grasses.

10. The plant according to claim 5 in which the mutated gene results in one or more of the following amino acid substitutions in the EPSPS enzyme in comparison with the wild-type sequence:

- (i) Leu₁₇₃ - Phe
- (ii) Gly₁₇₇ - Ala or Ile
- (iii) Thr₁₇₈ - Ile or Val or Leu
- 10 (iv) Ala₁₇₉ - Gly
- (v) Met₁₈₀ - Cys
- (vi) Arg₁₈₁ - Leu or Ser
- (vii) Pro₁₈₂ - Leu or Ser
- (viii) Ser₉₈ -Asp
- 15 (ix) Ser₂₅₅ -Ala
- (x) Leu₁₉₈ -Lys.

11. The plant according to claim 6 in which the mutated gene results in one or more of the following amino acid substitutions in the EPSPS enzyme in comparison with the wild-type sequence:

- (i) Leu₉₇ - Phe
- (ii) Gly₁₀₁ - Ala or Ile
- (iii) Thr₁₀₂ - Ile or Val or Leu
- (iv) Ala₁₀₃ - Gly
- 25 (v) Met₁₀₄ - Cys
- (vi) Arg₁₀₅ - Leu or Ser
- (vii) Pro₁₀₆ - Leu or Ser
- (viii) Ser₂₃ -Asp
- (ix) Ser₁₇₉ -Ala
- 30 (x) Leu₁₂₂ -Lys.

12. The plant according to claim 7 in which the mutated gene results in one or more of the following amino acid substitutions in the EPSPS enzyme in comparison with the wild-type sequence:

- 35 (i) Leu₁₆₉ - Phe
- (ii) Gly₁₇₃ - Ala or Ile

- (iii) Thr₁₇₄ - Ile or Val or Leu
- (iv) Ala₁₇₅ - Gly
- (v) Met₁₇₆ - Cys
- (vi) Arg₁₇₇ - Leu or Ser
- 5 (vii) Pro₁₇₈ - Leu or Ser
- (viii) Ser₉₄ -Asp
- (ix) Ser₂₅₁ -Ala
- (x) Leu₁₉₄ -Lys.

10 13. The plant according to claim 8 in which the mutated gene results in one or more of the following amino acid substitutions in the EPSPS enzyme in comparison with the wild-type sequence:

- (i) Leu₁₆₉ - Phe
- (ii) Gly₁₇₃ - Ala or Ile
- 15 (iii) Thr₁₇₄ - Ile or Val or Leu
- (iv) Ala₁₇₅ - Gly
- (v) Met₁₇₆ - Cys
- (vi) Arg₁₇₇ - Leu or Ser
- (vii) Pro₁₇₈ - Leu or Ser
- 20 (viii) Ser₉₄ -Asp
- (ix) Ser₂₅₁ -Ala
- (x) Leu₁₉₄ -Lys.

25 14. A method for producing a non-transgenic herbicide resistant or tolerant plant comprising

- a. introducing into a plant cell a recombinagenic oligonucleobase to produce a mutant EPSPS gene; and
- b. identifying a cell having a mutated EPSPS gene, which cell has substantially normal growth as compared to a corresponding wild-type plant cell.

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15. A method for producing a non-transgenic herbicide resistant or tolerant plant comprising

- a. introducing into a plant cell a recombinagenic oligonucleobase to produce a mutant EPSPS gene; and

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b. identifying a cell having a mutated EPSPS gene, which encoded mutant EPSPS protein has substantially the same catalytic activity as compared to a corresponding wild-type EPSPS protein.

5 16. The method according to claim 14 or 15 in which the recombinagenic oligonucleobase is a mixed duplex nucleotide or a SSMOV.

17. The method according to claim 16 in which the mixed duplex nucleotide contains a first homologous region which has a sequence identical to the sequence of at
10 least 6 base pairs of the first fragment of the target EPSPS gene and a second homologous region which has a sequence identical to the sequence of at least 6 based pairs of a second fragment of the target EPSPS gene, and an intervening region which contains at least one nucleobase heterologous to the target EPSPS gene, which intervening region connects the first and second homologous region.

15 18. The method according to claim 14 or 15 in which the recombinagenic oligonucleobase is introduced by electroporation.

19. The method according to claim 14 or 15 which the mutant EPSPS gene
20 is mutated at one or more amino acid positions, said positions selected from the group consisting of Leu₁₇₃, Gly₁₇₇, Thr₁₇₈, Ala₁₇₉, Met₁₈₀, Arg₁₈₁, Pro₁₈₂, Ser₉₈, Ser₂₅₅ and Leu₁₉₈ in *Arabidopsis* or at an analogous amino acid residue in an EPSPS paralog.

20. The plant according to claim 19 in which the positions in the *Zea mays*
25 paralog are selected from the group consisting of Leu₉₇, Gly₁₀₁, Thr₁₀₂, Ala₁₀₃, Met₁₀₄, Arg₁₀₅, Pro₁₀₆, Ser₂₃, Ser₁₇₉ and Leu₁₂₂.

21. The plant according to claim 19 in which the positions in the *Brassica napus* paralog are selected from the group consisting of Leu₁₆₉, Gly₁₇₃, Thr₁₇₄, Ala₁₇₅, Met₁₇₆,
30 Arg₁₇₇, Pro₁₇₈, Ser₉₄, Ser₂₅₁ and Leu₁₉₄.

22. The plant according to claim 19 in which the positions in the *Petunia hybrida* are selected from the group consisting of Leu₁₆₉, Gly₁₇₃, Thr₁₇₄, Ala₁₇₅, Met₁₇₆,
Arg₁₇₇, Pro₁₇₈, Ser₉₄, Ser₂₅₁ and Leu₁₉₄.

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23. The plant according to claim 14 or 15 in which the plant is selected from the group consisting of corn, wheat, rice, barley, soybean, cotton, sugarbeet, oilseed rape, canola, flax, sunflower, potato, tobacco, tomato, alfalfa, poplar, pine, eukalyptus, apple, lettuce, peas, lentils, grape, turf grasses and *Brassica* sp.

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24. An isolated mutant EPSPS protein comprising the amino acid sequence depicted in SEQ ID NO:2, in which amino acid position Leu₁₇₃ is replaced with Phe, Gly₁₇₇ is replaced with Ala or Ile, Thr₁₇₈ is replaced with Ile or Val or Leu, Ala₁₇₉ is replaced with Gly, Met₁₈₀ is replaced with Cys, Arg₁₈₁ is replaced with Leu or Ser, Pro₁₈₂ is replaced with
10 Leu or Ser, Ser₉₈ is replaced with Asp, Ser₂₅₅ is replaced with Ala or Leu, Leu₁₉₈ is replaced with Lys, which mutant EPSPS protein has increased resistance or tolerance to a herbicide, which herbicide is a member of the phosphonomethylglycine family.

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DNA sequence:

cccttcatgtcittttagaaccacccattatctttcttagggcccaattgaaaaccacattttctttcacctaacc
 ccaaaagccttgacatgttgacgtgaacaccaaactaacacgtgcatactgccagtggttatgataaatgctcatacc
 ataccagagtcataagagtttttggttggtgaaagattgacggatgccttcttctcattttctaccaactccctccaaa
 cccaacaaaatgtttatattagcaaaagccgcaaaagtgtaaacgaaagttataaatttcattttctgtgatcttacgta
 attggaggaagatcaaaattttcaatccccattcttcgattgcttcaattgaagtttctccg

[transit peptide start]

ATGGCGCAAGTTAGCAGAATCTGCAATGGTGTGCAGAACCCATCTCTTATCTCCAATCTCTCGAAATCCAGTCAACGCA
 AATCTCCCTTATCGGTTTCTCTGAAGACGCAGCAGCATCCACGAGCTTATCCGATTTCTGTCGTCTGCGGGATTGAAGAA
 GAGTGGGATGACGTTAATTGGCTCTGAGCTTCGTCTCTTAAGGTCATGTCTTCTGTTTCCACGGCGGAG

[mature peptide starts]

AAAGCGTCGGAGATTGACTTCAACCCATTAGAGAAATCTCCGGTCTTATTAAGCTTCCTGGCTCCAAGTCTCTATCAA
 ATCGGATCCTGCTTCTCGCTGCTCTGTCTGAGGTATATATCACTTCGTTTCGTCTTCTCTGTAATCTGAACCTAGATT
 ATAAAGATTGATACTTTACCATTTTGTCTGGTTTTATAGGGAACAACGTAGTGGACAACCTGTTGAATAGCGATGAC
 ATCAATTACATGCTTGATGCGTTGAAGAGATTGGGACTTAATGTGGAACCTGACAGTGAAAATAATCGTGCTGTAGTTG
 AAGGATGTGGCGGGATATTCCAGCTTCCATAGATTCAAAGAGTGATATCGAAGTTTACCTCGGTAATGCAGGAACAGC
 AATGCGTCCACTTACCGCTGCGGTCACTGCTGCAGGTGGAACGCAAGGTAGATTGAAGGAGTTGATGCTTCTTGGTAT
 TTGATGTTTAAGGAATGGAGCTTTTGTGATGCTTTATGATCCATTTATTCCAGTTATGTGCTTGATGGGGTGCCTCGT
 ATGAGAGAAAGACCTATAGGGGATTGGTTGGTCTTAAGCAGCTTGGTGCTGATGTTGAATGTACTCTTGGAACTA
 ACTGCCCTCCTGTTCTGTCAACGCTAATGGTGGCCTTCCGGTGGAAGGTTAGATCTTGCAATGGCATGTGAATAT
 GTAATCTCGTTCCTTACTCTATGAACACTTGCAGAAATGTGTGTTTCATCATAGCCTTAGCTTGACAAGATTTAGTTTT
 TAATCTACTCTCAACGGATGGATCCTAAAATAGAATCGGATTTGGTGATTGGTTTTCTGTTCTCGATTACCGTTTTCTGTT
 GTATGATTTCTTGATTAACAATTAGGAGACATGTTATGCATTTGCAGGTGAAGCTTTCTGGATCAATTAGTAGTCAGTA
 CTTGACTGCTCTGCTCATGTCTGCTCCCTTAGCTCTTGGAGACGTCGAGATTGAGATTGTCGATAAATTAATTTCTGTT
 CCAATATGTTGAAATGACATTGAAGTTGATGGAACGTTTCGGGGTTAGTGTCGAGCATAGTGATAGCTGGGATCGTTTCT
 TTGTCAAGGGCGGGCAAAAATACAAGTAGGAGTTATTCTTTCTTCTTTCTGAAATCACATCCCTTAGCTTGACAAAT
 ATAATGACTAAAAGGTGAATGATTCAGGTCTCCGGTAATGCGTATGTAGAAGGTGATGCTTCTAGTGCATGTTATTTCT
 TTGGCTGGTGTGCCATTACCGGTGAACTGTACAGTCGAAGGTTGTGGAACCTACCAGCTTGACAGTAATATTTGTAC
 ACTGAATCATCGACGAGGCTGTTAAGTTTATAGTGAAATTCGTCTAGGTCAAAGTTTCATCTTTTGACAAGTTGTATAT
 AACATATTCGCAAGATTCTAAGCTCAATTTTGTGATGAATCTCTAGGGAGATGTAAATTCGCCGAGGTCTTGAGAA
 AATGGGATGTAAAGTGTCTTGACAGAGAACAGTGTGACTGTGACAGGACCACCTAGAGATGCTTTTGGAATGAGACAC
 TTGCGGGCTATTGATGTCAACATGAACAAAATGCCTGATGTAGCCATGACCTTGCCGTCGTTGCTCTCTTTGCTGACG
 GTCCAACCAACATTAGAGATGGTAAGTAAAAAGCTCTCTCTTATAATTAAGGTTTCTCAATATTCATGATCACTTAATT
 CTGTTTGGTTAATATAGTGGCTAGCTGGAGAGTAAAGGAGACAGAAAGGATGATTGCCATTTGCACAGAGCTTAGAAAA
 GTAAGAGATTCTTATCTCTCTCTTTCTGTCTCTTGACAGTGCTCATTCTAAGTAATTAGCTCATAAATTTGTGTGTTG
 TGTTGAGCTGGGAGCTACAGTGAAGAAGGTTGAGATTATTGTGTGATAACTCCGCCAAAAAGGTGAAAACGGCAGAG
 ATTGATACATATGATGATCATAGAATGGCAATGGCATTCTCTCTTGACGCTTGTGCTGATGTTCCAATCACCATCAACG
 ACTCTGGTTGCACAGGAAAACTTCCCCGACTACTTCCAAGTACTTGAAAGAATCACAAAGCACTAAacaataaaactc
 tgttttttcttctgatccaagctt

FIG. 1A

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Protein sequence:

MAQVSRICNGVQNPSLISNLSKSSQRKSPLSVSLKTQQHPRAYPISSSWGLKKSGMTLIGSELRLPKVMSSVSTAE
KASEIVLQPIREISGLIKLPGSKSLSNRILLALLAALSEGTTVVDNLLNSDDINYMLDALKRLGLNVETDSENNRAVV
EGCGGIFPASIDSKSDIELYLGNAGTAMRPLTAAVTAAGGNASYVLDGVPRMRERPIGDLVVGLKQLGADVECTLG
TNCPPVRVNANGGLPGGKVKLSGSISSQYL TALLMSAPLALGDVEIEIVDKLISVPYVEMTLKLMEFVGVSVEHSD
SWDRFFVKGGQKYKSPGNAYVEGDASSACYFLAGAAITGETVTVEGCGTTSLQGDVKFAEVLEKMGCKVSWTENS
TVTGPPRDAFGMRHLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETERMIAICTELRKL
GATVEEGSDYCVITPPKKVKTAEIDTYDDHRMAMAFSLAACADVPITINDSGCTRKTFPDYFQVLERITKH

FIG. 1B

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Arabidopsis thaliana wild type sequence:

Position	173	174	175	176	177	178	179	180	181	182	183
	L	G	N	A	G	T	A	M	R	P	L
	CTC	GGT	AAT	GCA	GGA	ACA	GCA	ATG	CGT	CCA	CTT

Arabidopsis thaliana mutant sequences:

Name	
A ₁₇₇	CTC GGT AAT GCA GCA ACA GCA ATG CGT CCA CTT L G N A A T A M R P L
I ₁₇₈	CTC GGT AAT GCA GCA ATA GCA ATG CGT CCA CTT L G N A G I A M R P L
A ₁₇₇ I ₁₇₈	CTC GGT AAT GCA GCA ATA GCA ATG CGT CCA CTT L G N A A I A M R P L
I ₁₇₈ S ₁₈₂	CTC GGT AAT GCA GGA ATA GCA ATG CGT TCA CTT L G N A G I A M R S L
A ₁₇₇ S ₁₈₂	CTC GGT AAT GCA GCA ACA GCA ATG CGT TCA CTT L G N A A T A M R S L
A ₁₇₇ I ₁₇₈ S ₁₈₂	CTC GGT AAT GCA GCA ATA GCA ATG CGT TCA CTT L G N A A I A M R S L
V ₁₇₈ S ₁₈₂	CTC GGT AAT GCA GGA GTA GCA ATG CGT TCA CTT L G N A G V A M R S L
L ₁₇₈ S ₁₈₂	CTC GGT AAT GCA GGA TTA GCA ATG CGT TCA CTT L G N A G L A M R S L
A ₁₇₇ V ₁₇₈	CTC GGT AAT GCA GCA GTA GCA ATG CGT CCA CTT L G N A A V A M R P L
A ₁₇₇ L ₁₇₈	CTC GGT AAT GCA GCA TTA GCA ATG CGT CCA CTT L G N A A L A M R P L

FIG.2

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10	20	30	40	50	60	70	80	90	
1	ATGGCGCAAGTTAGCAGAATCTGCAATGGTGTGCAGAACCCAT	...	CTCTATCTCCAAATCTCTGAAATCCAGTCAACGAAATCTCC	...	CTTATCGG				atepspcDNA .SEQ
1	ATGGCGCAATCTAGCAGAATCTGCCATGGCGTGCAGAACCCATGTGTATCATCTCCAAATCTCCAAATCCAAACAAATCAGC	...	TTTCTCCG						bnepsDNA .SEQ
1	ATGGCACAATTAACAACATGGCTCAAGGGATACAAACCCTTA	...	ATCCAATTCCAATTTCCATAAACCCCAAGTTCCTAAATCTTCAAGTTTCTTG						petaroacDNA .SEQ
1	GCGG	zmepsps .SEQ
100	110	120	130	140	150	160	170	180	190
95	TTTCT	...	CTGAAGACGACGAGCATCCACGAGCTTATCCGATTCGTGCTGTGGGATTGAAGAAGTGGGATGACGTTAATTTGGCTCTGAGCTTCG						atepspcDNA .SEQ
98	TCCTCC	...	TTGAAGACGATCAGC	...	CTCGAGCTT	...	CTTCGTGGGATTGAAGAAGTGGGATGCTAAACGGTCTCTGTAATTCG		bnepsDNA .SEQ
98	TTTTTGGATCTAAAAAACTGAAAAATTCAGCAAT	...	CTATGTTGGTTTGAAGAAAGATTCAATTTT	...	TATGCAAAAGTTTTCG				petaroacDNA .SEQ
5	GTGCCGAGG	...
200	210	220	230	240	250	260	270	280	290
192	TCCTCTTAAGGTCATGCTTCTGTTTCCACGGCGGAGAAAGGTCGGAGATTGTAATCAACCCATTAGAGAAATCTCCGGTCTTATTAAAGTTCCTGGC								atepspcDNA .SEQ
180	CCCGGTTAAGGTAACAGCTTCTGTTCCACGTCGAGAAAGCTTCAGAGATTGCTTCAACCAATCAGACAAATCTCGGGTCTCATTAAGCTACCCGGA								bnepsDNA .SEQ
180	TTCCCTTAGGATTTACGATCAGTGCTACAGCAGACAGAGCCCTCTGAGATAGTGTGCAACCCATTAAAGAGATTTCAAGGCACTGTAAATTTGCCTGGC								petaroacDNA .SEQ
14	AGATCGTGTCTGACGCCATCAAGGAGATCTCCGGCACCGTCAAGCTGCCGGGG				zmepsps .SEQ
300	310	320	330	340	350	360	370	380	390
292	TCCAAGTCTCTATCAATCGGATCCTGCTTCTCGCTGCTGTCTGAGGGAACAACCTGTAGTGGACAACCTTGTGAATAGCGATGACATCAATTACATGC								atepspcDNA .SEQ
280	TCCAAATCTCTCTCAATCGGATCCTCCTTCTGCGCTCTATCTGAGGGAACCTACTGTAGTGGACAACCTTGTGAACAGTGTGACATCAACTACATGC								bnepsDNA .SEQ
280	TCTAAATCATTATCTAAATAGAATTCCTTCTTGTGCTGCTTATCTGAAGGAACAACCTGAGTGTGACAAATTTACTAAGTAGTGTGATATTCATTACATGC								petaroacDNA .SEQ
67	TCCAAGTGGCTTTCCAAACCGGATCCTCTACTCGCGCCCTGTCCGAGGGGACAACAGTGTGTGAACCTGCTGAACAGTGGAGATGTCACATACATGC								zmepsps .SEQ
400	410	420	430	440	450	460	470	480	490
392	TTGATGCGTTGAAGAGATTGGGACTTAATGTGGAAACTGACAGTGAATAATTCGTGCTGTAGTTGAAGGATGTGGGGGATATCCAGCTTCCATAGA								atepspcDNA .SEQ
380	TTGATGCGTTGAAGAGCTGGGGCTTAACGTGGAAACGTGACAGTGTAAACAACCGTGGCTGTGTGAAGGATGCGGTGGAAATATCCAGCTTCCATAGA								bnepsDNA .SEQ
380	TTGGTGGCTTGAAGACACTTGGACTGCATGTAGAAGAGATAGTGAACCAACGAGCTGTGTGAAGGTTGTGGTGGGCTTTCCCTGTGGTAAAGA								petaroacDNA .SEQ
167	TCGGGGCTTGAAGACTCTTGGTCTCTCTGTGCGAAGCGGACAAAGCTGCCAAAGAGCTGTAGTTGTGGCTGTGGTGGAAAGTTCACAGTTG	...	AGGA						zmepsps .SEQ

FIG.3A

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500	510	520	530	540	550	560	570	580	590	atepspscDNA. SEQ
492	TTCAAAGAGTGATATCGAACTTACCTCGGTAAATGCAGGAACAGCAATGGCTCCACTTACCGCTGCGGTCACTGCTGAGGTTGGAACGCAAGTTATGTG									bnepscDNA. SEQ
480	TTCCAAGAGTGATATGAGTTGTACCTTGGGAATGCAGGAACAGCCATGGCTCCACTACCGCTGCAGTTACAGCTGCAGGTGGCAACGCGAGTTATGTGTA									petaroacDNA. SEQ
480	GTCCAAGGAAGAAATTCAACTGTTCCCTTGGAAATGCAGGAACAGCAATGCGGCCACTAACAGCAGCAGTTACTGTAGCTGGTGGAAATTCAGGTTATGTGTA									zmepps. SEQ
264	TGCTAAAGAGGAAGTGACGCTCTTCTTGGGGAATGCTGGAACTGCAATGCGGCCCATTTGACAGCAGCTGTTACTGCTGCTGGTGGAAATGCAACTTACGTG									
600	610	620	630	640	650	660	670	680	690	atepspscDNA. SEQ
592	CTTGATGGGGTGCCTCGTATGAGAGAAAGACCTATAGGGGATTGGTTGGTCTTAAGCAGCTTGGTGTGATGTTGAATGTACTCTTGGAACTTAAC									bnepscDNA. SEQ
580	CTTGATGGGGTGCCTAGAAATGAGGGAAGACCTATAGGAGATTGGTTGGTCTTAAGCAGCTTGGTGTGATGTTGAGTGTACTCTTGGCACTTAAC									petaroacDNA. SEQ
580	CTTGATCGAGTTCCTCGAATGAGAGAGACCAATTAGTGAATTTGGTTGATGGTCTTAACAGCTTGGTGCAGAGTTGATTGTTCCCTTGGTACGAAAT									zmepps. SEQ
364	CTTGATGGAGTACCAAGNAATGAGGGAGAGACCCATTGGCGACTTGGTTGCGGATTGAAGCAGCTTGGTGCAGATGTTGATTGTTCCCTTGGCACTGACT									
700	710	720	730	740	750	760	770	780	790	atepspscDNA. SEQ
692	GCCCTCCTGTTGCTGTCAACGCTAATGGTGGCTTCCCGGTGGAAAGGTGAAGCTTCTGGATCAATTAGTAGTCAGTACTTGACTGCTGCTCATGTC									bnepscDNA. SEQ
680	GTCCTCCTGTTGCTGTCAATGCTAATGGTGGCTTCCCGGTGGAAAGGTGAAGCTTCTGGATCGATCAGTAGTCAGTACTTGACTGCCCTCCTCATGCG									petaroacDNA. SEQ
680	GTCCTCCTGTTGCAATTGTGAGCAAGGAGGCTTCTCTGGAGGGAAGGTCAAGCTCTCTGGATCCATTAGCAGCCAACTTGCATGCTGCTGCTTATGGC									zmepps. SEQ
464	GCCCACTGTTGCTGTCAATGGAATCGGAGGGCTACCTGGTGGCAAGGTCAAGCTGTCTGGCTCCATCAGCAGTCAGTACTTGAGTGCCTTGCTGATGGC									
800	810	820	830	840	850	860	870	880	890	atepspscDNA. SEQ
792	TGCTCCCTTAGCTCTTGGAGACGTCGAGATTGAGATTGTCGATAAATTAATTTCTGTCCATATGTTGAATGACATTGAAGTTGATGGAACTGTTTCGGG									bnepscDNA. SEQ
780	AGCTCCTTAGCTCTTGGAGACGTCGAGATTGAGATCAATTGATAAATGATATCTGTCCATATGTTGAATGACATTGAAGTTGATGGAGCGTTTGTGGT									petaroacDNA. SEQ
780	TGCTCCACTGGCTTAGGAGATGGAGATTGAAATCATTTGACAAACTAATAGTGTACCTTATGTCGAGATGACATTGAAGTTGATGGAGCGATTGGT									zmepps. SEQ
564	TGCTCCTTTGGCTCTTGGGGATGGAGATTGAAATCATTTGATAAATTAATCTCCATCCGTACGTCGAAATGACATTGAGATTGATGGAGCGTTTGTGGT									
900	910	920	930	940	950	960	970	980	990	atepspscDNA. SEQ
892	GTTAGTGTGAGCATAGTATAGCTGGGATCGTTTCTTTGTCAAGGGGGGCAAAAATACAAGTCTCCGGTAATGGGTATGTAGAGGTGATGCTTCTA									bnepscDNA. SEQ
880	GTTAGTGCCGAGCATAGTATAGCTGGGATCGTTTCTTTGTCAAGGGGGTCAAAAATACAAGTCCGCTGGTAATGCTTATGTAGAGGTGATGCTTCTA									petaroacDNA. SEQ
880	ATTTCTGTGGAGCAGATAGTATAGCTGGGACAGGTTCTTTGTCCGAGAGGTCAGAAAATACAAGTCTCCCTGGAAAGCTTTTGTGGAAGGTGATGCTTCAA									zmepps. SEQ
664	GTGAAAGCAGAGCATTTCTGATAGCTGGGACAGATTCTACATTAGGGAGGTCAAAAATACAAGTCCCTTAAAAATGCTTATGTTGAAGGTGATGCCCTCAA									

FIG.3B

[illegible]

FIG. 3C

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10	20	30	40	50	60	70	80	90	100																																	
1	MAQVSRICNGVNP	- SLISNL	SKSSQRKSP	LSVSLKTQ	HPRAYP	ISSWGLK	KSGMTL	IGSELR	PLKWNSSV	STAEKASE	IVLQPIRE	ISGLIK	PGSKLSLN	atepsps. PRO																											
1	MAQSSRICHGQNP	CVITISNL	SKSNQNKSP	FVSLSKTHQ	PRASSMGL	KSGTML	NGSVIR	PKVKITASV	STSEKASE	IVLQPIRE	ISGLIK	PGSKLSLN	bnepsps. PRO																											
1	MAQINMAQGIQTL	- NPNSNF	HKPQVP	KSSSFL	VFGSKK	LKNSA	NSMLVL	KDSIF	MQKFC	SFRISAS	VATAQ	PKSEIVLQPIKE	ISGTIVKLPGSKLSLN	petaraoa. PRO																										
1	AG	zmepps. PRO																										
110	120	130	140	150	160	170	180	190	200	210																																
104	RILLAA	SEGT	TVVDNL	LNSSD	INMIL	DALKRL	GLNVE	TDSENN	RAWEG	CGGIF	PASID	SKSDIEL	YLG	VAGT	AMRPL	TAAVTA	AGGNASY	VLDG	VPRMR	ERP	ICDLV	atepsps. PRO																				
100	RILLAA	SEGT	TVVDNL	LNSSD	INMIL	DALKRL	GLNVE	TDSENN	RAWEG	CGGIF	PASID	SKSDIEL	YLG	VAGT	AMRPL	TAAVTA	AGGNASY	VLDG	VPRMR	ERP	IGDLV	bnepsps. PRO																				
100	RILLAA	SEGT	TVVDNL	LNSSD	INMIL	GALKTL	GLHVE	EDSAN	QRAV	VEGCGGL	FPVG	KEEIQ	FL	GNAGT	AMRPL	TAAVT	VAGNSRY	VLDG	VPRMR	ERP	ISDLV	petaraoa. PRO																				
29	RILLAA	SEGT	TVVDNL	LNSSD	VHML	GALRTL	GLSVE	ADKAA	KRAV	VGGCGK	FPV	- EDA	KEEV	QL	FL	GNAGT	AMRPL	TAAVTA	AGGNATY	VLDG	VPRMR	ERP	IGDLV	zmepps. PRO																		
220	230	240	250	260	270	280	290	300	310	320																																
214	VGLKQ	LAD	VECT	LTG	NCPP	RVN	ANGGL	PGGK	VKL	SGS	ISSQ	L	TALL	MSAP	LAL	GDVE	IEI	VDKL	ISVP	VVEM	TL	KMER	FGV	SVEH	SDMD	RFF	VKG	GQ	KYK	SPGNA	atepsps. PRO											
210	VGLKQ	LAD	VECT	LTG	NCPP	RVN	ANGGL	PGGK	VKL	SGS	ISSQ	L	TALL	MAAP	LAL	GDVE	IEI	IDKL	ISVP	VVEM	TL	KMER	FGV	SAEH	SDMD	RFF	VKG	GQ	KYK	SPGNA	bnepsps. PRO											
210	DGLKQ	LAD	VECT	LTG	NCPP	RVN	SKGGL	PGGK	VKL	SGS	ISSQ	L	TALL	MAAP	LAL	GDVE	IEI	IDKL	ISVP	VVEM	TL	KMER	FGV	SVEH	SDMD	RFF	VKG	GQ	KYK	SPGNA	petaraoa. PRO											
138	VGLKQ	LAD	VECT	LTG	NCPP	RVN	GIGGL	PGGK	VKL	SGS	ISSQ	L	SALL	MAAP	LAL	GDVE	IEI	IDKL	ISVP	VVEM	TL	KMER	FGV	KAEH	SDMD	RFF	VKG	GQ	KYK	SPGNA	zmepps. PRO											
330	340	350	360	370	380	390	400	410	420	430																																
324	YVEGD	ASSA	CYF	LAGA	AIT	GET	TV	VEG	CGT	TS	LQ	GDV	KFAE	VLE	KMG	CKV	SW	TENS	SV	TV	GT	PP	RD	AF	GM	RHL	RA	ID	VNM	NK	MPD	VAM	TL	AV	VAL	FAD	GP	TT	IRD	VAS	MRV	atepsps. PRO
320	YVEGD	ASSA	CYF	LAGA	AIT	GET	TV	VEG	CGT	TS	LQ	GDV	KFAE	VLE	KMG	CKV	SW	TENS	SV	TV	GT	PP	RD	AF	GM	RHL	RA	ID	VNM	NK	MPD	VAM	TL	AV	VAL	FAD	GP	TT	IRD	VAS	MRV	bnepsps. PRO
320	FVEGD	ASSA	CYF	LAGA	AVT	GET	TV	VEG	CGT	NS	LQ	GDV	KFAE	VLE	KMG	AEV	TENS	SV	TV	KG	PP	SS	SG	RHL	RA	ID	VNM	NK	MPD	VAM	TL	AV	VAL	YAD	GP	TT	IRD	VAS	MRV	petaraoa. PRO		
248	YVEGD	ASSA	CYF	LAGA	AIT	GET	TV	VEG	CGT	TS	LQ	GDV	KFAE	VLE	KMG	AKV	TW	TETS	SV	TV	GT	PP	PE	FG	RHL	KA	ID	VNM	NK	MPD	VAM	TL	AV	VAL	FAD	GP	TT	IRD	VAS	MRV	zmepps. PRO	
440	450	460	470	480	490	500	510	520																																		
434	KETER	MAI	ACT	EL	RKL	GAT	VEE	GDY	CV	IT	PP	KV	KV	TAE	ID	YDD	HR	MA	F	SLA	AC	AD	VP	IT	IND	SG	TR	KT	FP	DY	FQ	V	LE	R	IT	KH	atepsps. PRO					
430	KETER	MAI	ACT	EL	RKL	GAT	VEE	GDY	CV	IT	PP	KV	KV	TAE	ID	YDD	HR	MA	F	SLA	AC	AD	VP	IT	IND	SG	TR	KT	FP	DY	FQ	V	LE	R	IT	KH	bnepsps. PRO					
430	KETER	MAI	ACT	EL	RKL	GAT	VEE	GDY	CV	IT	PP	KE	LV	TD	ID	YDD	HR	MA	F	SLA	AC	AD	VP	IT	IND	PG	CT	RK	TF	PN	V	FD	V	LQ	Q	YS	KH	petaraoa. PRO				
358	KETER	MAI	ACT	EL	RKL	GAT	VEE	GDY	CV	IT	PP	KE	LV	TD	ID	YDD	HR	MA	F	SLA	AC	AE	VP	IT	IND	PG	CT	RK	TF	FP	DY	FD	V	L	ST	F	V	KN	zmepps. PRO			

FIG.4

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<u>Oligo Name</u>	<u>Oligo Sequence (5'→3')</u>
ATEPS-A ₁₇₇	CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGGACGCATTGCTGTTGCTGCATTACCGAG
ATEPS-AI	CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGGACGCATTGCTATTGCTGCATTACCGAG
ATEPS-IS	CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGAACGCATTGCTATTCCTGCATTACCGAG
ATEPS-AS	CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGAACGCATTGCTGTTGCTGCATTACCGAG
ATEPS-AIS	CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGAACGCATTGCTATTGCTGCATTACCGAG
ATEPS-I ₁₇₇	CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGGACGCATTGCTGTTATTGCATTACCGAG
ATEPS-VS	CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGAACGCATTGCTACTCCTGCATTACCGAG
ATEPS-LS	CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGAACGCATTGCTAATCCTGCATTACCGAG
ATEPS-AV	CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGGACGCATTGCTACTGCTGCATTACCGAG
ATEPS-AL	CGTTTCCACCTGCAGCAGTGACCGCAGCGGTAAGTGGACGCATTGCTAATGCTGCATTACCGAG

FIG.5

SUBSTITUTE SHEET (RULE 26)

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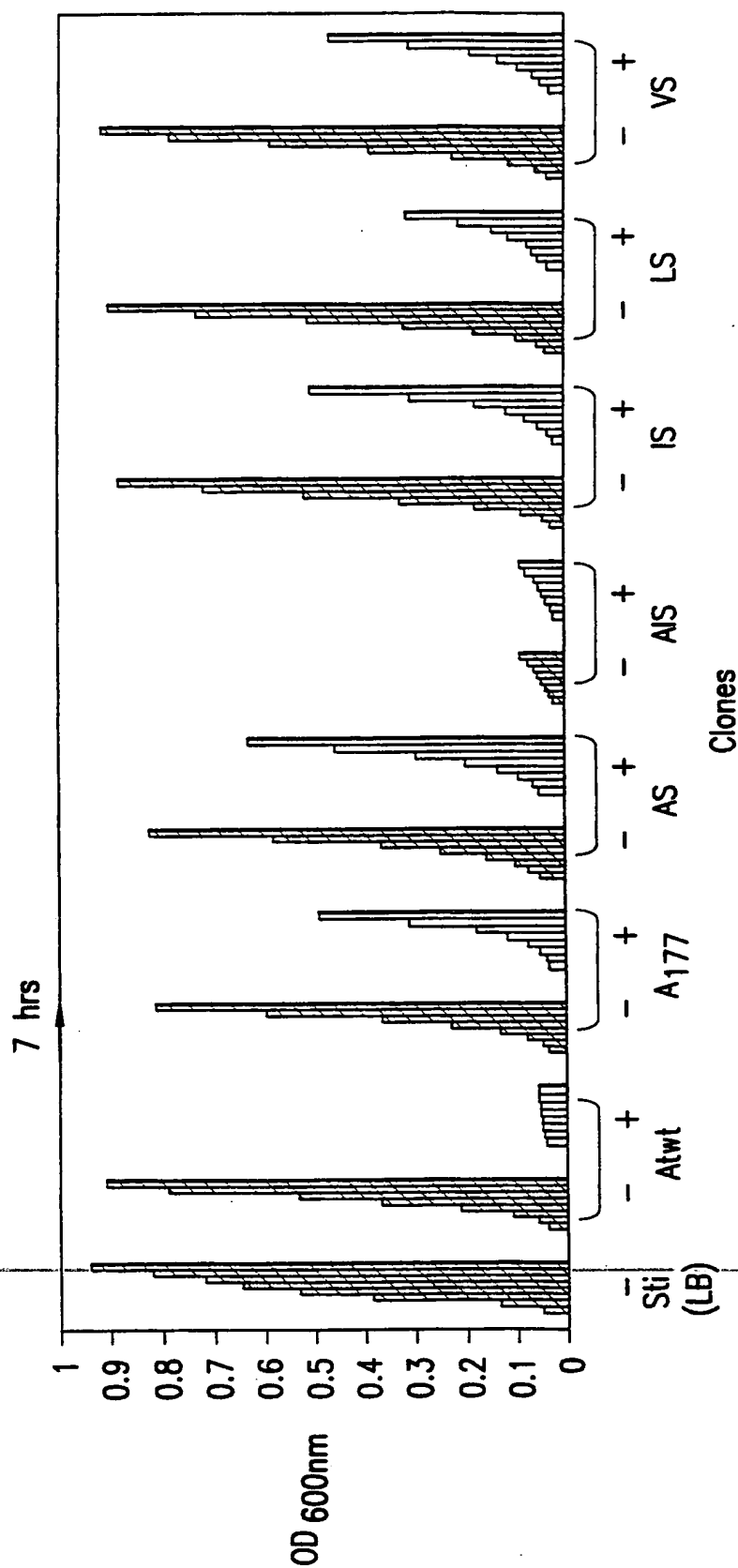


FIG.6

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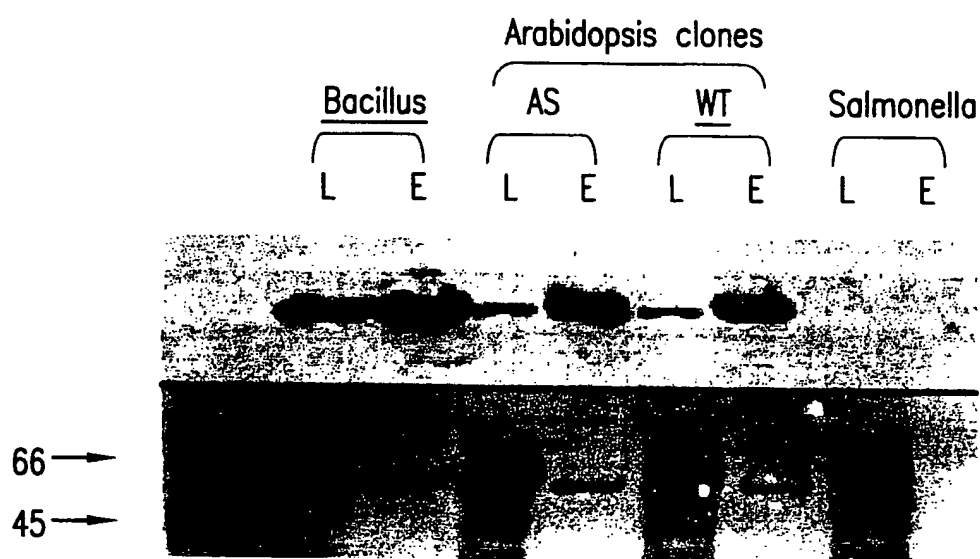


FIG.7

SEQUENCE LISTING

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<120> NON-TRANSGENIC HERBICIDE RESISTANT PLANTS

<130> 7991-086-228

<150> 60/158,027

<151> 1999-10-07

<150> 60/173,564

<151> 1999-12-30

<160> 44

<170> FastSEQ for Windows Version 3.0

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ggttgggtgaa	agatttgacg	gatgccttct	tctcatttct	caccaactcc	ctccaaaccc	240
aacaaaatgt	ttatattagc	aaagcgcgca	aagtgtaaac	gaaagtttat	aaatttcatt	300
tctgtgatct	tacgtaattg	gaggaagatc	aaaattttca	atccccattc	ttcgattgct	360
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<212> PRT

<213> Arabidopsis thaliana

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Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser
35          40          45
Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg
50          55          60
Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Glu Lys Ala Ser Glu
65          70          75          80
Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu Ile Lys Leu Pro
85          90          95
Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu Ala Ala Leu Ser
100         105         110
Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn Ser Asp Asp Ile Asn
115         120         125
Tyr Met Leu Asp Ala Leu Lys Arg Leu Gly Leu Asn Val Glu Thr Asp
130         135         140
Ser Glu Asn Asn Arg Ala Val Val Glu Gly Cys Gly Gly Ile Phe Pro
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Ala Ser Ile Asp Ser Lys Ser Asp Ile Glu Leu Tyr Leu Gly Asn Ala
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Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr Ala Ala Gly Gly
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Asn Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro
195         200         205
Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly Ala Asp Val Glu
210         215         220
Cys Thr Leu Gly Thr Asn Cys Pro Pro Val Arg Val Asn Ala Asn Gly
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245         250         255
Tyr Leu Thr Ala Leu Leu Met Ser Ala Pro Leu Ala Leu Gly Asp Val
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Glu Ile Glu Ile Val Asp Lys Leu Ile Ser Val Pro Tyr Val Glu Met
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Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Val Glu His Ser Asp
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 Met Gly Cys Lys Val Ser Trp Thr Glu Asn Ser Val Thr Val Thr Gly
 370 375 380
 Pro Pro Arg Asp Ala Phe Gly Met Arg His Leu Arg Ala Ile Asp Val
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 450 455 460
 Pro Lys Lys Val Lys Thr Ala Glu Ile Asp Thr Tyr Asp Asp His Arg
 465 470 475 480
 Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Ile Thr
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 1 5 10

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 1 5 10

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 1 5 10

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<400> 22
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<210> 24

<211> 1944

<212> DNA

<213> *Petunia hybrida*

<400> 24

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<210> 25

<211> 1335

<212> DNA

<213> *Zea mays*

<400> 25

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<210> 26

<211> 516

<212> PRT

<213> Brassisca napus

<400> 26

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Val Ser Leu Lys Thr His Gln Pro Arg Ala Ser Ser Trp Gly Leu Lys
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Lys Ser Gly Thr Met Leu Asn Gly Ser Val Ile Arg Pro Val Lys Val
50      55      60
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65      70      75      80
Pro Ile Arg Glu Ile Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser
85      90      95
Leu Ser Asn Arg Ile Leu Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr
100      105      110
Val Val Asp Asn Leu Leu Asn Ser Asp Asp Ile Asn Tyr Met Leu Asp
115      120      125
Ala Leu Lys Lys Leu Gly Leu Asn Val Glu Arg Asp Ser Val Asn Asn
130      135      140
Arg Ala Val Val Glu Gly Cys Gly Gly Ile Phe Pro Ala Ser Leu Asp
145      150      155      160
Ser Lys Ser Asp Ile Glu Leu Tyr Leu Gly Asn Ala Gly Thr Ala Met
165      170      175
Arg Pro Leu Thr Ala Ala Val Thr Ala Ala Gly Gly Asn Ala Ser Tyr
180      185      190
Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro Ile Gly Asp Leu
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Val Val Gly Leu Lys Gln Leu Gly Ala Asp Val Glu Cys Thr Leu Gly
210      215      220
Thr Asn Cys Pro Pro Val Arg Val Asn Ala Asn Gly Gly Leu Pro Gly
225      230      235      240
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245      250      255
Leu Leu Met Ala Ala Pro Leu Ala Leu Gly Asp Val Glu Ile Glu Ile
260      265      270
Ile Asp Lys Leu Ile Ser Val Pro Tyr Val Glu Met Thr Leu Lys Leu
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Met Glu Arg Phe Gly Val Ser Ala Glu His Ser Asp Ser Trp Asp Arg
290      295      300
Phe Phe Val Lys Gly Gly Gln Lys Tyr Lys Ser Pro Gly Asn Ala Tyr
305      310      315      320
Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Gly Ala Ala
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 Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Lys Met Gly Cys Lys
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 370 375 380
 Ala Phe Gly Met Arg His Leu Arg Ala Val Asp Val Asn Met Asn Lys
 385 390 395 400
 Met Pro Asp Val Ala Met Thr Leu Ala Val Val Ala Leu Phe Ala Asp
 405 410 415
 Gly Pro Thr Thr Ile Arg Asp Val Ala Ser Trp Arg Val Lys Glu Thr
 420 425 430
 Glu Arg Met Ile Ala Ile Cys Thr Glu Leu Arg Lys Leu Gly Ala Thr
 435 440 445
 Val Glu Glu Gly Ser Asp Tyr Cys Val Ile Thr Pro Pro Ala Lys Val
 450 455 460
 Lys Pro Ala Glu Ile Asp Thr Tyr Asp Asp His Arg Met Ala Met Ala
 465 470 475 480
 Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Val Thr Ile Lys Asp Pro
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 Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val Leu Glu Ser
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 Ile Thr Lys His
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<210> 27

<211> 516

<212> PRT

<213> Petunia hybrida

<400> 27

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 Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val
 35 40 45
 Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile
 50 55 60
 Ser Ala Ser Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln
 65 70 75 80
 Pro Ile Lys Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser
 85 90 95
 Leu Ser Asn Arg Ile Leu Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr
 100 105 110
 Val Val Asp Asn Leu Leu Ser Ser Asp Asp Ile His Tyr Met Leu Gly
 115 120 125
 Ala Leu Lys Thr Leu Gly Leu His Val Glu Glu Asp Ser Ala Asn Gln
 130 135 140
 Arg Ala Val Val Glu Gly Cys Gly Gly Leu Phe Pro Val Gly Lys Glu
 145 150 155 160
 Ser Lys Glu Glu Ile Gln Leu Phe Leu Gly Asn Ala Gly Thr Ala Met
 165 170 175
 Arg Pro Leu Thr Ala Ala Val Thr Val Ala Gly Gly Asn Ser Arg Tyr
 180 185 190
 Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro Ile Ser Asp Leu
 195 200 205

Val Asp Gly Leu Lys Gln Leu Gly Ala Glu Val Asp Cys Phe Leu Gly
 210 215 220
 Thr Lys Cys Pro Pro Val Arg Ile Val Ser Lys Gly Gly Leu Pro Gly
 225 230 235 240
 Gly Lys Val Lys Leu Ser Gly Ser Ile Ser Ser Gln Tyr Leu Thr Ala
 245 250 255
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 260 265 270
 Ile Asp Lys Leu Ile Ser Val Pro Tyr Val Glu Met Thr Leu Lys Leu
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 Met Glu Arg Phe Gly Ile Ser Val Glu His Ser Ser Ser Trp Asp Arg
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 Val Thr Gly Gly Thr Ile Thr Val Glu Gly Cys Gly Thr Asn Ser Leu
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 Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Lys Met Gly Ala Glu
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 Val Thr Trp Thr Glu Asn Ser Val Thr Val Lys Gly Pro Pro Arg Ser
 370 375 380
 Ser Ser Gly Arg Lys His Leu Arg Ala Ile Asp Val Asn Met Asn Lys
 385 390 395 400
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 Gly Pro Thr Ala Ile Arg Asp Val Ala Ser Trp Arg Val Lys Glu Thr
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 Glu Arg Met Ile Ala Ile Cys Thr Glu Leu Arg Lys Leu Gly Ala Thr
 435 440 445
 Val Glu Glu Gly Pro Asp Tyr Cys Ile Ile Thr Pro Pro Glu Lys Leu
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 465 470 475 480
 Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Val Thr Ile Asn Asp Pro
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<210> 28

<211> 444

<212> PRT

<213> Zea mays

<400> 28

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 Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
 65 70 75 80

Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
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 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
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 Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
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 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
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 Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
 145 150 155 160
 Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
 165 170 175
 Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
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 Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
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 225 230 235 240
 Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
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 Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
 260 265 270
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<212> PRT
<213> Petunia hybrida

<400> 39

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gcggtcctc aggatttttt cgaaagctta tttaaagt 38

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 44
gaaagcgtcg gagattgtac 20

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/27941

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : A01H 1/06; C07H 21/04; C12N 5/04, 9/00, 15/01, 15/09, 15/29, 15/87
US CL : 435/183, 410, 413, 418; 530/370; 536/23.1, 23.2; 800/276, 278, 300,300.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 435/183, 410, 413, 418; 530/370; 536/23.1, 23.2; 800/276, 278, 300,300.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	US 6,066,786 ROSE-FRICKER) 23 May 2000 (23.05.00), entire reference.	1-4, 9
Y		5-8, 10-13
X	GORLANI et al. A glyphosate-resistant 5-enol-pyruvyl-shikimate-3-phosphate synthase confers tolerance to a maize cell line. Plant science 1992, Vol. 85, pages 9-15, entire reference.	1-4, 9
Y		5-8, 10-13
Y	PADGETTE et al. Site-directed mutagenesis of a conserved region of the 5-enolpyruvylshikimate-3-phosphate synthase active site. J. biol. chem. 25 November 1991, Vol. 266, No. 33, pages 22364-22369, especially Table 1, page 22365.	14-23
Y	US 5,756,325 A (KMEC) 26 May 1998 (26.05.98), entire reference.	14-23
Y,P	US 6,004,804 A (KUMAR et al) 21 December 1999 (21.12.99), entire reference.	14-23

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier application or patent published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

21 November 2000 (21.11.2000)

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703)305-3230

Date of mailing of the international search report

JAN 19 2001

Authorized officer

David Kruse

Telephone No. 703-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/27941

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐
☒

- The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/27941

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-23, drawn to a non-transgenic herbicide resistant plant that expresses a mutant EPSPS gene product and a method of producing said plant.

Group II, claim(s) 24, drawn to an isolated mutant EPSPS protein containing amino acid substitutions at specific sequence sites.

The inventions listed as Groups I and II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The isolated mutant EPSPS protein of Group II lacks a corresponding technical feature with the transgenic-herbicide resistant plant and the method of producing said plant of Group I. The isolated mutant EPSPS protein of Group II requires multiple amino acid substitution and the EPSPS expressed in the transgenic plant of Group I only requires one amino acid substitution.

Continuation of B. FIELDS SEARCHED Item 3:

- (1) EAST (USPAT, Derwent, JPO, EPO); natural glyphosate resistance, non-transgenic herbicide resistance, recombinogenic oligonucleobase, site directed mutation [in] plant(s).
- (2) STN (BIOSIS, AGRICOLA, EMBASE, CAPLUS); EPSPS Mutant/Mutation [in] plant(s), Natural glyphosate resistance.
- (3) Sequence Search of SEQ ID NO:2

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